

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2003, 23:29:38 ; Search time 15.375 Seconds
(without alignments)
8.256 Million cell updates/sec

Title: US-09-967-003-2
Perfect score: 15
Sequence: 1 RTR 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32717 seqs, 42310958 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2.6/ptodata/1/1aa/5B_COMB.pep:*

2: /cgn2.6/ptodata/1/1aa/6A_COMB.pep:*

3: /cgn2.6/ptodata/1/1aa/6B_COMB.pep:*

4: /cgn2.6/ptodata/1/1aa/PCTUS.Comb.pep:*

5: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query	Match Length	DB ID	Description
1	15	100.0	3	4	US-09-521-365A-2
2	15	100.0	4	2	US-09-521-365A-61
3	15	100.0	4	2	US-09-521-365A-68
4	15	100.0	5	1	US-08-366-591-14
5	15	100.0	5	2	US-08-348-355-8
6	15	100.0	5	2	US-08-463-965-8
7	15	100.0	5	3	US-08-465-965-8
8	15	100.0	5	3	US-09-01-124-7
9	15	100.0	5	3	US-09-395-341-7
10	15	100.0	5	4	US-09-521-365A-3
11	15	100.0	5	4	US-09-546-483-6
12	15	100.0	5	4	US-09-822-177-6
13	15	100.0	6	1	US-08-264-002-11
14	15	100.0	6	1	US-08-064-111C-4
15	15	100.0	6	3	US-09-12-120-8
16	15	100.0	6	3	US-09-395-341-8
17	15	100.0	6	3	US-09-257-218-17
18	15	100.0	6	3	US-09-311-760-17
19	15	100.0	6	4	US-09-561-750-54
20	15	100.0	6	4	US-09-227-721-54
21	15	100.0	6	4	US-08-865-579-17
22	15	100.0	6	4	US-09-122-14-8
23	15	100.0	6	4	US-10-050-743-17
24	15	100.0	7	2	US-08-310-912A-90
25	15	100.0	7	3	US-08-841-059-90
26	15	100.0	7	3	US-09-301-085-90
27	15	100.0	7	5	PCT-US95-04589-90

ALIGNMENTS

RESULT 1
US-09-521-365A-2
; Sequence 2, Application US/09521365A
; Patent No. 6310041
; GENERAL INFORMATION:
; APPLICANT: Haddox, Jeffrey
; APPLICANT: Blalock, James
; APPLICANT: Matteo, William
; TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC USES TH
; FILE REFERENCE: 92750/57
; CURRENT APPLICATION NUMBER: US/09/521, 365A
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 60/123, 409
; FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2 LENGTH: 2
; TYPE: PRT
; LENGTH: 3
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: description of artificial sequence: amino acid
; OTHER INFORMATION: sequence of complement peptide inhibitor of
; OTHER INFORMATION: neutrophils; used as a monomer, dimer, and tetramer
US-09-521-365A-2

Query Match 100.0%; Score 15; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RTR 3	1 RTR 3
Db	1	1
	1 RTR 3	1 RTR 3

RESULT 2
US-08-589A-61
; Sequence 61, Application US/08685589A
; Patent No. 6310041
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Pennie & Edmonds LLP
; STREET: 115 Avenue of the Americas

CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,589A
 FILING DATE: 24-JUL-1996
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 8067-026-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-750-9090
 TELEFAX: 212-869-9741
 INFORMATION FOR SEQ ID NO: 68
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 STRANDEDNESS: unknown
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLogy: No. 5916872 Relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..4
 OTHER INFORMATION: /product= "Beta-turn"
 US-08-685-589A-61

Query Match 100.0%; Score 15; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 RTR 3	111
Db	2 RTR 4	

RESULT 3
 US-08-685-589A-68
 Sequence 68, Application US/08685589A
 Patent No. 5916872

GENERAL INFORMATION:
 APPLICANT: Chang, Conway

APPLICANT: Gu, Leo
 APPLICANT: Chen, Jie
 TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
 TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
 NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penile & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,591
 FILING DATE: 29-DEC-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 2222-0002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0860
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: peptide

RESULT 4
 US-08-366-591-14
 Sequence 14, Application US/08366591
 Patent No. 5603021

GENERAL INFORMATION:
 APPLICANT: Davis G., Claude
 APPLICANT: Guay, Gordon G.
 TITLE OF INVENTION: Method for Generating Proteolytic
 TITLE OF INVENTION: Enzymes Specific Against a Selected Peptide Sequence
 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,591
 FILING DATE: 29-DEC-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 2222-0002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0860
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: peptide

STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,966
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/7348,353
 FILING DATE: 30-NOV-1994
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/247,572
 FILING DATE: 23-MAY-1994
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/03725
 FILING DATE: 04-MAY-1992
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/695,613
 FILING DATE: 03-MAY-1991
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson, David
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-097CIP1D1V2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-342-1684
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 TYPE: amino acid
 LENGTH: 5 amino acids
 MOLECULE TYPE: peptide
 US-08-465-966-8

Query Match: 100.0%; Score: 15; DB: 3; Length: 5;
 Best Local Similarity: 100.0%; Pred. No: 2.5e+05;
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 1 RTR 3
 Db 2 RTR 4

RESULT 8
 US-09-012-126-7
 Sequence 7, Application US/09012126
 Patent No: 6017735
 GENERAL INFORMATION:
 APPLICANT: Haddox, Jeffrey
 APPLICANT: Pfister, Robert
 APPLICANT: Blalock, James
 APPLICANT: Matteo, Villain
 TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC USES THEREFOR
 FILE REFERENCE: 92750/57
 CURRENT APPLICATION NUMBER: US/09/521,365A
 CURRENT FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: US 60/123,409
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 3
 LENGTH: 5
 TYPE: PRT
 FEATURE:
 ORGANISM: artificial sequence

TITLE OF INVENTION: Materials and methods for intracellular transport and
 TITLE OF INVENTION: their uses
 FILE REFERENCE: 49406
 CURRENT APPLICATION NUMBER: US/09/012,126
 CURRENT FILING DATE: 1998-01-22
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 7
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-012-126-7
 Query Match: 100.0%; Score: 15; DB: 3; Length: 5;
 Best Local Similarity: 100.0%; Pred. No: 2.5e+05;
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 9
 US-09-395-344-7
 Sequence 7, Application US/09395344
 Patent No: 6253398
 GENERAL INFORMATION:
 APPLICANT: O'Hare and Elliott
 TITLE OF INVENTION: Materials and methods for intracellular transport and
 TITLE OF INVENTION: their uses
 FILE REFERENCE: 42408
 CURRENT APPLICATION NUMBER: US/09/395,344
 CURRENT FILING DATE: 1995-09-13
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 7
 LENGTH: 5
 TYPE: PRT
 FEATURE:
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-395-344-7
 Query Match: 100.0%; Score: 15; DB: 3; Length: 5;
 Best Local Similarity: 100.0%; Pred. No: 2.5e+05;
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 10
 US-09-521-365A-3
 Sequence 3, Application US/09521365A
 Patent No: 6310041
 GENERAL INFORMATION:
 APPLICANT: Haddox, Jeffrey
 APPLICANT: Pfister, Robert
 APPLICANT: Blalock, James
 APPLICANT: Matteo, Villain
 TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC USES THEREFOR
 FILE REFERENCE: 92750/57
 CURRENT APPLICATION NUMBER: US/09/521,365A
 CURRENT FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: US 60/123,409
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 3
 LENGTH: 5
 TYPE: PRT
 FEATURE:
 ORGANISM: artificial sequence

OTHER INFORMATION: Description of Artificial Sequence: amino acid
 OTHER INFORMATION: description of artificial sequence: amino acid
 OTHER INFORMATION: sequence of complementary peptide inhibitor of
 OTHER INFORMATION: neutrophils; used as a monomer
 US-09-521-365A-3
 Query Match: 100.0%; Score: 15; DB: 4; Length: 5;
 Best Local Similarity: 100.0%; Pred. No: 2.5e+05;
 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

RESULT 11

US-09-546-483-6

QY 1 RTR 3
Db 1 RTR 3

Sequence 6, Application US/09546483

PATENT NO. 5559019

GENERAL INFORMATION:

APPLICANT: GUIL, JIAN-FANG

APPLICANT: FU, XIANG-DONG

TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ

STREET: 1880 Century Park East, Fifth Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #11.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/264,002

FILING DATE: 22-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: TUMARKIN PH.D., LISA A.

REGISTRATION NUMBER: P-38-347

REFERENCE/DOCKET NUMBER: PD3590

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/455-5100

FAX: 619/455-5110

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..6

RESULT 12

US-09-823-177-6

QY 1 RTR 3
Db 1 RTR 3

Sequence 6, Application US/09823177

PATENT NO. 6451601

GENERAL INFORMATION:

APPLICANT: Baetge, Ed

APPLICANT: Wong, Shou

APPLICANT: Dupraz, Philippe

APPLICANT: Thorens, Bernard

TITLE OF INVENTION: TRANSIENTLY IMMORTALIZED CELLS FOR USE IN GENE THERAPY

PRIOR APPLICATION NUMBER: 09/546,483

PRIOR APPLICATION NUMBER: 17811-011

PRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 5

TYPE: PRY

ORGANISM: Herpes simplex type 1 virus

Query Match

Best Local Similarity 100.0%; Score 15; DB 4; Length 5;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

US-08-264-002-11

QY 1 RTR 3
Db 2 RTR 4

Sequence 4, Application US/0806411C

PATENT NO. 5688760

GENERAL INFORMATION:

APPLICANT: Kemp, Bruce E.

APPLICANT: Nicholson, Geoffrey C.

APPLICANT: Martin, Thomas J.

APPLICANT: Fenton, Anna J.

APPLICANT: Hammonds, R. Glenn

TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT BONE RESORPTION

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flair, Hohbach, Test, Albritton & Herbert,

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

RESULT 14

US-08-064-111C-4

QY 1 RTR 3
Db 1 RTR 3

Sequence 4, Application US/0806411C

PATENT NO. 5688760

GENERAL INFORMATION:

APPLICANT: Kemp, Bruce E.

APPLICANT: Nicholson, Geoffrey C.

APPLICANT: Martin, Thomas J.

APPLICANT: Fenton, Anna J.

APPLICANT: Hammonds, R. Glenn

TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT BONE RESORPTION

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flair, Hohbach, Test, Albritton & Herbert,

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

RESULT 15

US-08-264-002-11

Search completed: September 9, 2003, 23:36:07
 Job time : 17.375 secs

MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/064,111C
 FILING DATE: 12-AUG-1993
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU91/00580
 FILING DATE: 13-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PK9567
 FILING DATE: 19-NOV-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PK3179
 FILING DATE: 13-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-58456/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 731-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277-99
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 US-08-064,111C-4

Query Match Score 15; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 RTR 3
 Db 1 RTR 3

RESULT 15

US-09-012-126-8
 ; Sequence 8, Application US/09012126
 ; Patient No. 6017735
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Hare and Elliott
 ; TITLE OF INVENTION: Materials and methods for intracellular transport and
 ; FILE REFERENCE: their uses
 ; CURRENT APPLICATION NUMBER: US/09/012,126
 ; CURRENT FILING DATE: 1998-01-22
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 6
 ; TYPE: PRT
 ; FEATURE: ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: peptide
 ; US-09-012-126-8

Query Match Score 15; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 QY 1 RTR 3
 Db 1 RTR 3

PT analogues
 XX
 PS Claim 3; Page 149; 160pp; English.
 XX
 CC This sequence represents a beta-turn region used in a peptide of the invention. The peptides are cyclic peptides (I), which have: (a) an amphiphilic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta turn region (TR); (b) a net positive charge at physiological pH; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad spectrum antimicrobials, specifically for use against *E. coli*, *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus faecium* and penicillin-resistant *Streptococcus pneumoniae*. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from clinical uses, (I) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachyplesin and protegrin type peptides), (I) and are more effective, with better bioavailability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant strains.
 XX
 Sequence 4 AA:
 Query Match 100.0%; Score 15; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 1 RTR 4
 XX
 RESULT 2
 AAW52417
 ID AAW52417 standard; peptide; 4 AA.
 XX
 AC AAW52417;
 XX
 DT 01-JUL-1998 (first entry)
 DE Beta-turn region used in cyclic peptide of the invention.
 KW preservative; amphiphilic anti-parallel beta-sheet region; plant disease.
 XX
 OS Synthetic.
 XX
 PN W09803192-A1.
 XX
 PD 29-JAN-1998.
 XX
 PR 23-JUL-1997; 97WO-US12974.
 XX
 PR 24-JUL-1996; 96US-0685589.
 XX
 PA (INVR-) INTRABIOTICS PHARM INC.
 XX
 PI Chang C, Chen J, Gu L;
 XX
 DR WPI; 1998-120472/11.
 XX
 PT New cyclic peptide(s) with antimicrobial activity - contain amphiphilic beta-sheet, loop and beta-turn regions, have better activity, bioavailability and protease resistance than linear analogues
 PT
 PS Claim 3; Page 149; 160pp; English.
 XX
 CC This sequence represents a beta-turn region used in a peptide of the invention. The peptides are cyclic peptides (I), which have: (a) an amphiphilic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta turn (C), (ii) having net positive charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C).
 CC AAV09554 to AAV09683 and AAV17301 to AAV17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-spectrum antimicrobials (biostatic or biocidal), effective against bacteria, yeast (e.g. *Candida* species), fungi and protozoa. Particularly they are used to control *Escherichia coli*, *Pseudomonas aeruginosa*,
 CC

CC a beta-turn region (TR); (b) a net positive charge at physiological pH; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad spectrum antimicrobials, specifically for use against *E. coli*, *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus faecium* and penicillin-resistant *Streptococcus pneumoniae*. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from clinical uses, (I) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachyplesin and protegrin type peptides), (I) and are more effective, with better bioavailability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant strains.
 XX
 Sequence 4 AA:
 Query Match 100.0%; Score 15; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 1 RTR 3
 XX
 RESULT 3
 ID AAY09621 standard; Peptide; 4 AA.
 XX
 AC AAY09621;
 XX
 DT 21-JUL-1999 (first entry)
 DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:68.
 XX
 KW Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic; biocidal; bacteria; yeast; *Candida* species; fungi; protozoa;
 KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
 KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
 KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
 KW penicillin-resistant *streptococcus pneumoniae*; cosmetic.
 OS Synthetic.
 XX
 PN W09821879-A1.
 XX
 PD 06-MAY-1999.
 XX
 PR 27-OCT-1997; 97WO-US19557.
 XX
 PR 27-OCT-1997; 97WO-US19557.
 XX
 PA (INVR-) INTRABIOTICS PHARM INC.
 XX
 PI Chang C, Chen J, Gu L;
 XX
 DR WPI; 1999-312941/26.
 XX
 PT Antimicrobial cyclic peptides with amphiphilic beta-sheet region
 XX
 PS Claim 3; Page 150; 167pp; English.
 XX
 CC The present invention describes cyclic Peptides (I); (I) comprising an amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta turn (C), (ii) having net positive charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C).
 CC AAV09554 to AAV09683 and AAV17301 to AAV17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-spectrum antimicrobials (biostatic or biocidal), effective against bacteria, yeast (e.g. *Candida* species), fungi and protozoa. Particularly they are used to control *Escherichia coli*, *Pseudomonas aeruginosa*,

CC vancomycin-resistant *Enterococcus faecium*, methicillin-resistant
 CC *Staphylococcus aureus* and penicillin-resistant *Streptococcus*
 CC *pneumoniae*. (I) are used to treat or prevent infections, in animals or
 CC plants, also as preservatives and disinfectants for medical equipment,
 CC foods, cosmetics, optionally as mixtures or in combination with other
 CC antimicrobials. Compared with linear analogues, (I) are more effective
 CC with better bioavailability and/or serum half-life (better resistance
 CC to proteolysis, allowing lower doses and making them more suitable for
 CC oral delivery). Since (I) are structurally related to naturally
 CC occurring antimicrobial peptides, they are less likely to induce
 CC oral delivery). Since (I) are structurally related to naturally
 CC occurring antimicrobial peptides, they are less likely to induce
 CC development of resistant strains.

SQ sequence 4 AA:

Query Match	100.0%	Score 15;	DB 20;	Length 4;
Best Local Similarity	100.0%	Pred. No.	9.3e+05;	
Matches	3;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Oy	1 RTR 3			
Db	111	2 RTR 4		

RESULT 4

AY09614	AY09614 standard; peptide; 4 AA.
AC	AY09614;
XX	
XX	21-JUL-1999 (first entry)
DE	Antimicrobial cyclic peptide beta-turn region SEQ ID NO:61.
XX	
KW	Cyclic Peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
KW	biocidal; bacteria; yeast; <i>Candida</i> species; fungi; protozoa;
KW	<i>Escherichia coli</i> ; <i>Pseudomonas aeruginosa</i> ; infection; preservative;
KW	<i>Vancomycin</i> -resistant <i>Enterococcus faecium</i> ; disinfectant; food;
KW	methicillin-resistant <i>Staphylococcus aureus</i> ; medical equipment;
KW	penicillin-resistant <i>Streptococcus pneumoniae</i> ; cosmetic.
OS	Synthetic.
XX	
PN	WO9921879-A1.
XX	
PD	06-MAY-1999.
XX	
PP	27-OCT-1997; 97WO-US19557.
PR	
XX	
PA	(INVR-) INTRABIOTICS PHARM INC.
PI	Chang C, Chen J, Gu L;
XX	
DR	WPI; 1999-312941/26.
XX	
PT	Antimicrobial cyclic peptides with amphiphilic beta-sheet region
PS	Claim 3; Page 150; 167PP; English.
XX	
CC	The present invention describes cyclic peptides (I): (i) comprising an CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and CC a beta-turn (C); (ii) having net positive charge at physiological pH; CC and (iii) including at least one basic amino acid (aa) in (B) or (C). CC AAY09614 to AY09683 and AY17301 to AY17385 represent specifically CC claimed cyclic peptides and peptide segments. (I) are broad spectrum CC antimicrobials (biostatic or biocidal), effective against bacteria, CC yeast (e.g. <i>Candida</i> species), fungi and protozoa. Particularly they CC are used to control <i>Escherichia coli</i> , <i>Pseudomonas aeruginosa</i> , CC <i>Vancomycin</i> -resistant <i>Enterococcus faecium</i> , methicillin-resistant CC <i>Staphylococcus aureus</i> and penicillin-resistant <i>Streptococcus</i> CC <i>pneumoniae</i> . (A) are used to treat or prevent infections, in animals or CC plants, also as preservatives and disinfectants for medical equipment,

CC foods, cosmetics, optionally as mixtures or in combination with other
 CC antimicrobials. Compared with linear analogues, (I) are more effective
 CC with better bioavailability and/or serum half-life (better resistance
 CC to proteolysis, allowing lower doses and making them more suitable for
 CC oral delivery). Since (I) are structurally related to naturally
 CC occurring antimicrobial peptides, they are less likely to induce
 CC development of resistant strains.

SQ sequence 4 AA:

Query Match	100.0%	Score 15;	DB 20;	Length 4;
Best Local Similarity	100.0%	Pred. No.	9.3e+05;	
Matches	3;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Oy	1 RTR 3			
Db	111	1 RTR 3		

RESULT 5

AY09614	AY09614 standard; peptide; 5 AA.
AC	AY09614;
XX	
XX	12-JAN-1996 (first entry)
DE	Streptokinase-binding Plasmin B chain peptide.
XX	
KW	Streptokinase; plasmin B; affinity chromatography; purification;
KW	isolation.
OS	Homo sapiens.
XX	
PN	GB2284422-A.
XX	
PD	07-JUN-1995.
XX	
PF	29-NOV-1994; 94GB-0024112.
XX	
PR	29-NOV-1993; 93GB-0024473.
XX	
PA	(OXFO-) OXFORD RES SUPPORT CO LTD.
XX	
PT	Cederholm-Williams SA;
XX	
DR	WPI; 1995-196178/26.
XX	
PT	New peptide sequences from plasmin B chain - able to bind other PT proteins esp. streptokinase, useful for affinity purifcn.
XX	
PS	Claim 3; Page 6; 14PP; English.
XX	
CC	AY09614 to AY09683 and AY17301 to AY17385 represent specifically CC claimed cyclic peptides and peptide segments. (I) are broad spectrum CC antimicrobials (biostatic or biocidal), effective against bacteria, CC yeast (e.g. <i>Candida</i> species), fungi and protozoa. Particularly they CC are used to control <i>Escherichia coli</i> , <i>Pseudomonas aeruginosa</i> , CC <i>Vancomycin</i> -resistant <i>Enterococcus faecium</i> , methicillin-resistant CC <i>Staphylococcus aureus</i> and penicillin-resistant <i>Streptococcus</i> CC <i>pneumoniae</i> . (A) are used to treat or prevent infections, in animals or CC plants, also as preservatives and disinfectants for medical equipment,

CC foods, cosmetics, optionally as mixtures or in combination with other
 CC antimicrobials. Compared with linear analogues, (I) are more effective
 CC with better bioavailability and/or serum half-life (better resistance
 CC to proteolysis, allowing lower doses and making them more suitable for
 CC oral delivery). Since (I) are structurally related to naturally
 CC occurring antimicrobial peptides, they are less likely to induce
 CC development of resistant strains.

SQ sequence 5 AA:

Query Match	100.0%	Score 15;	DB 16;	Length 5;
Best Local Similarity	100.0%	Pred. No.	9.3e+05;	
Matches	3;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Oy	1 RTR 3			
Db	111	1 RTR 3		

RESULT 6

AY09614	AY09614 standard; peptide; 5 AA.
AC	AY09614;
XX	
XX	12-JAN-1996 (first entry)
DE	Streptokinase-binding Plasmin B chain peptide.
XX	
KW	Streptokinase; plasmin B; affinity chromatography; purification;
KW	isolation.
OS	Homo sapiens.
XX	
PN	GB2284422-A.
XX	
PA	(OXFO-) OXFORD RES SUPPORT CO LTD.
XX	
PT	Cederholm-Williams SA;
XX	
DR	WPI; 1995-196178/26.
XX	
PT	New peptide sequences from plasmin B chain - able to bind other PT proteins esp. streptokinase, useful for affinity purifcn.
XX	
PS	Claim 3; Page 6; 14PP; English.
XX	
CC	AY09614 to AY09683 and AY17301 to AY17385 represent specifically CC claimed cyclic peptides and peptide segments. (I) are broad spectrum CC antimicrobials (biostatic or biocidal), effective against bacteria, CC yeast (e.g. <i>Candida</i> species), fungi and protozoa. Particularly they CC are used to control <i>Escherichia coli</i> , <i>Pseudomonas aeruginosa</i> , CC <i>Vancomycin</i> -resistant <i>Enterococcus faecium</i> , methicillin-resistant CC <i>Staphylococcus aureus</i> and penicillin-resistant <i>Streptococcus</i> CC <i>pneumoniae</i> . (A) are used to treat or prevent infections, in animals or CC plants, also as preservatives and disinfectants for medical equipment,

KW ciliated respiratory epithelial cell; filamentous haemagglutinin; FHA;
 KW RGD region; cerebral endothelial cell; inflammation; antibiotic therapy;
 KW infection; meningitis; septic arthritis; endophthalmitis.
 XX
 OS Synthetic.
 XX
 PN US5932217-A.
 XX
 PD 03-AUG-1999.
 XX
 30-NOV-1994; 94US-0348353.
 XX
 PR 03-MAY-1991; 91US-0695613.
 PR 04-MAY-1992; 92WO-US03725.
 PR 23-MAY-1994; 94US-0247572.
 PR 14-JUL-1994; 94US-0140136.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Masure HR, Tuomonen E;
 XX
 DR WPI; 1999-443571/37.
 XX
 Peptides inhibiting the adhesion between leukocytes and endothelial
 PT cells, useful for treating inflammation
 XX
 Claim 1; Column 75; 82PP; English.
 PS
 The specification describes Peptides which inhibit adhesion between
 CC leukocytes and endothelial cells, and peptides which inhibit adhesion
 CC between bacteria (*Bordetella pertussis*) and ciliated respiratory
 CC epithelial cells. The specification also describes an immunoactive
 composition comprising a polypeptide portion of *Bordetella pertussis*
 CC filamentous haemagglutinin (FHA) containing no RGD region or containing
 CC an amino acid sequence altered in the RGD region, where the polypeptide
 CC portion elicits antibodies which do not cross-react with cerebral
 CC endothelial cells. The peptides and methods are useful for reducing
 CC inflammation during the course of antibiotic therapy of infectious
 CC diseases such as meningitis, septic arthritis and endophthalmitis.
 CC The present sequence represents a peptide of the invention.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 XX
 Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 15; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTR 3
 Db 2 RTR 4
 RESULT 9
 AAY07209
 ID AAY07209 standard; peptide; 5 AA.
 XX
 AC AAY07209;
 XX
 DT 16-JUL-1999 (first entry)
 DE Adenoviral NLS peptide #5 for transfection vector.
 XX
 Peptide vector; transfection; adenovirus; fiber protein; hydrophobic;
 KW veterinary medicine; gene therapy; antibacterial; anticancer; ribozyme;
 KW human; immunogen; vaccination; antisense; nuclear localisation signal.
 XX
 OS Synthetic.
 OS Adenovirus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /label= Thr, Ala, Ser, Ser-Lys
 XX

XX
 PN FR2770537-A1.
 XX
 PD 07-MAY-1999.
 XX
 PR 03-NOV-1997; 97FR-0013771.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 XX
 PI Chroboczek J, Fender P;
 XX
 DR WPI; 1999-290555/25.
 XX
 PT peptide vector for transfection of cells, containing adenoviral
 PT fiber peptide
 XX
 PS Claim 3; Page 22; 33PP; French.
 XX
 CC The invention relates to a peptide vector for transfection with a
 CC "chemical" comprising, apart from the chemical, at least one
 CC transfection peptide derived, entirely or in part, from an adenoviral
 CC fiber protein and at least one region consisting of at least 50
 CC hydrophobic amino acids (aa), e.g. Ala, Val, Phe, Ile, Leu, Pro and Met.
 CC The chemical is a nucleic acid, protein, peptide or pharmaceutically
 CC active agent. The transfection agent is selected from the nuclear
 CC localisation sequences AAY07205-Y07210 and the hydrophobic region from
 CC AAY07211-Y07212. The Peptide vectors are used, in human or veterinary
 CC medicine, to treat or prevent diseases, particularly in gene therapy,
 CC e.g. of inherited diseases, viral infections, or as antibacterial and
 CC anticancer agents, also as immunogens for vaccination. Where the
 CC "chemical" is nucleic acid, it may encode a therapeutic protein,
 CC antisense sequence or ribozyme.
 XX
 SQ Sequence 5 AA;
 SQ
 Query Match 100.0%; Score 15; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTR 3
 Db 3 RTR 5
 RESULT 10
 AAB21218
 ID AAB21218 standard; peptide; 5 AA.
 XX
 AC AAB21218;
 XX
 DT 23-FEB-2001 (first entry)
 DE Synthetic complementary peptide.
 XX
 KW Polymorphonuclear leukocyte; PMN; ophthalmological; antiinflammatory;
 KW PMN chemotractant antagonist; N-acetyl-PGP; N-acetyl-PGx; N-methyl-PCP;
 KW neutrophil inhibitor; eye disease; alkali-injured eye;
 KW chemically injured eye; inflammatory eye disease.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 5
 FT /note= "C-terminal amide."
 XX
 PN WO20051621-A2.
 XX
 PD 14-SEP-2000.
 XX
 PP 08-MAR-2000; 2000WO-US06062.

XX	PR	09-MAR-1999;	PS	Disclosure; page 12; 40pp; English.	
XX	PA	(HADD/.) HADDOX J L.	XX		
XX	PA	(BLA/.) BLALOCK J E.	CC	polypeptide (Ia) having the transport function of herpes viral VP22	
XX	PA	(PFTS/.) PFISTER R R.	CC	protein or HIV TAR protein and polypeptide (Ib) having cell	
XX	PA	(VILL/.) VILLAIN M.	CC	immortalisation activity, telomerase specific activity or telomerase	
XX	PT	Haddox JL; Blalock JE, Pfister RR, Villain M;	CC	gene activation activity. (I) having (Ib) with cell immortalisation	
XX	PT	DR	CC	activity is useful for transiently immortalising a cell (Cl). (I) having	
XX	WPI;	2000-611433/58.	CC	(Ib) with telomerase specific activity is useful for transiently	
XX	PR	Pharmaceutical composition for treating eye diseases, comprises a	CC	telomerase a cell (Cl2). Two fusion proteins, with one comprising (Ib)	
XX	PR	peptide having sequence complementary to a specified sequence -	CC	having cell immortalisation activity and other comprising (Ib) having	
XX	PS	Claim 3; Page 36; 42pp; English.	CC	telomerase specific activity are together useful for increasing the	
XX	CC	The present sequence is a synthetic complementary peptide which is an	CC	replicative activity of a cell (C3). Where the cells (Cl), (C2) and (C3)	
CC	CC	anti-acetyl-PGP. It is therefore useful for inhibiting PMN polarisation,	CC	are not abundant and are difficult to obtain in pure form in primary	
CC	CC	chemotaxis and infiltration into tissue activated by neutrophil	CC	culture and includes normal somatic cells suitable for cell therapy,	
CC	CC	chemotactant such as N-acetyl- ω -Pep, N-acetyl-PGX, N-methyl-PGP, or	CC	the cells are not permanently immortalised and are not viraly infected,	
CC	CC	small peptide chemotactants containing proline and glycine. It may	CC	but upon removal of the exogenous immortalising or telomerase (I) are	
CC	CC	be used for treating eye diseases for e.g. alkali-injured eye,	CC	suitable for transplantation and use in cell therapy. The present	
CC	CC	chemically injured eye and inflammatory eye disease. The present	CC	sequence represents a peptide which is used in the exemplification of	
XX	CC	sequence is used as a monomer.	XX	the present invention.	
XX	SO	Sequence 5 AA:	SO	Sequence 5 AA:	
QY	Query Match	100.0%; Score 15; DB 21; Length 5;	QY	Query Match	100.0%; Score 15; DB 21; Length 5;
Db	Best Local Similarity	100.0%; Pred. No. 9.3e+05;	Db	Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Db	Matches	3; Conservative 0%; Mismatches 0;	Db	Matches	3; Conservative 0%; Mismatches 0;
Db	Indels	0;	Db	Indels	0;
Db	Gaps	0;	Db	Gaps	0;
Db	QY	1 RTR 3	Db	1 RTR 3	QY
Db	Db	1 RTR 3	Db	1 RTR 3	Db
RESULT 11			RESULT 12		
XX	AAV24246		XX	AAV67519	
XX	ID	AAV24246 standard; Peptide; 5 AA.	XX	ID	AAV67519 standard; peptide; 5 AA.
XX	AC		XX	AC	
XX	AAV24246;		XX	AAV67519;	
XX	DT	08-FEB-2001 (first entry)	XX	30-MAY-2000 (first entry)	
XX	DE	Transport activity peptide #4.	XX	DE	FHA peptide inhibiting leukocyte adhesion to endothelial cells.
XX	KW	Human; telomerase; hTERT; PCR primer; immortalised cell; gene therapy;	XX	KW	FHA; blood-brain barrier; filamentous hemagglutinin; endothelial cell;
XX	KW	cell therapy; herpes viral VP22 protein; HIV; TAR protein; herpesvirus;	XX	KW	complement C3b; factor X; integrin receptor CR3; leukocyte migration;
XX	KW	cell immortalisation activity; telomerase specific activity.	XX	KW	bacterial adhesion; brain cancer; acquired immune deficiency syndrome;
XX	KW	OS Herpesvirus.	XX	KW	Parkinson's disease; Alzheimer's disease; anticancer; anti-inflammatory;
XX	OS	W020061617-A2.	XX	OS	anti-inflammatory; anticancer; antiviral; antimicrobacterial; anti-neurodegeneration.
XX	PD	19-OCT-2000.	XX	OS	Bordetella pertussis.
XX	PF	12-APR-2000; 2000WO-US09775.	XX	PN	US6015560-A.
XX	PR	12-APR-1999; 99US-018893.	XX	PD	18-JAN-2000.
XX	PR	10-APR-2000; 2000US-0546269.	XX	PF	06-JUN-1995; 95US-0465966.
XX	PA	(MODE-) MODEX THERAPEUTIQUES SA.	XX	PR	30-NOV-1994; 94US-0348353.
XX	PA	Baetge EE, Wong S, Dupraz P, Thorens B;	PR	04-MAY-1992; 92WO-US3725.	
XX	PR	WPI; 2000-665115/64.	PR	03-MAY-1991; 91US-0595613.	
XX	PT	Fusion proteins with cell immortalization and telomerase specific	PR	23-MAY-1994; 94US-0247572.	
PT	PT	activity are useful for increasing replicative capacity of normally	XX	PA (UYRQ) UNIV RCKKEPELLER.	
PT	PT	quiescent cells such as somatic cells to produce cells suitable for	XX	PA Masure HR, Tuomanen E;	
PT	PT	cell therapy	XX	DR WPI; 2000-181133/16.	
XX	XX	Compositions containing antibody to filamentous hemagglutinin; used	XX	XX	
PT	PT	e.g. to increase permeability of the blood-brain barrier and to inhibit	PT	PT	
PT	PT	inflammation or bacterial adhesion	PT	PT	
PS	PS	Claim 4; Column 77; 82pp; English.	PS	PS	

XX
 CC The invention provides a novel pharmaceutical composition for increasing
 CC the permeability of the blood-brain barrier to a molecule (1). The
 CC composition comprises (1) and an antibody to FHA (filamentous
 CC hemagglutinin) which binds to endothelial cells in brain blood vessels,
 CC increasing permeability. FHA contains polypeptide regions with binding
 CC properties similar to those of complement C3b1, factor X and integrin
 CC receptor CR3, and some anti-FHA antibodies are competitive inhibitors
 of these materials, i.e. they reduce leukocyte migration or bacterial
 CC adhesion. The compositions are used to improve delivery of (1) to the
 CC brain, e.g. where (1) is used to treat brain cancer, acquired immune
 CC deficiency syndrome, epilepsy, Parkinson's or Alzheimer's diseases or
 CC other neurological diseases. Other antibodies directed against
 CC particular regions of FHA are used to treat inflammation (caused by
 CC microbial infection or auto-immune disease), also to prevent adhesion of
 CC *Bordetella pertussis* to respiratory endothelial cells. Sequences
 CC AAY67516-522 represent FHA peptides that inhibit adhesion between
 CC leukocytes and endothelial cells.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTR 3
 DB 2 RTR 4

RESULT 13
 AAE28114
 ID AAE28114 standard; peptide; 5 AA.
 XX
 AC AAE28114;
 XX
 DT 13-DEC-2002 (first entry)
 DE Human immunoglobulin G1 (IgG1) mutant peptide (residues 385-389) #1.
 XX
 KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia;
 KW vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;
 KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;
 KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;
 KW virucide; mutant; nutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT Misc-difference 2
 FT Misc-difference 3
 FT Misc-difference 4
 FT Misc-difference 5
 XX
 PN WO200250919-A2.
 XX
 PD 08-AUG-2002.
 XX
 PR 12-DEC-2001; 2001WO-US48432.
 XX
 PR 12-DEC-2000; 2000US-224884P.
 PR 09-MAY-2001; 2001US-289760P.
 XX
 PA (MEDT) MEDIMMUNE INC.
 PT Dall'Acqua W, Johnson LS, Ward ES;
 XX
 DR WPI; 2002-666925/71.

XX
 PT Modified immunoglobulins useful in the treatment of autoimmune
 PT diseases, comprises at least one amino acid modification relative to a
 PT wild-type immunoglobulin constant domain
 XX
 PS Example; Page 145; 147pp; English.
 XX
 CC The invention relates to a modified immunoglobulin (IgG1) which comprises
 CC an IgG constant domain having at least one amino acid modification. The
 CC immunoglobulins are used in the treatment or prevention of a disease or
 CC disorder by passive immunotherapy for vaccinating a subject and for in
 vivo diagnosis of a subject. The disease and disorders include a gamma
 CC globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-
 CC host, lymphoid malignancies and passive immunotherapies and also for the
 CC treatment of various systemic infections. The present sequence is human
 CC immunoglobulin G1 (IgG1) mutant peptide (residues 385-389). This peptide
 CC is used in the exemplification of the invention.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTR 3
 DB 1 RTR 3

RESULT 14
 ABB09212
 ID ABB09212 standard; peptide; 5 AA.
 XX
 AC ABB09212;
 XX
 DT 08-JUL-2002 (first entry)
 DE Glycoprotein cleavage site peptide SEQ ID NO:10.
 XX
 KW Vaccine; viral infection; immunity; immune response; glycoprotein;
 KW pathogenic virus; HIV; influenza virus; respiratory syncytial virus;
 KW herpes simplex virus; human papilloma virus; Ebola virus; Marburg virus;
 KW hepatitis A virus; hepatitis B virus; hepatitis C virus;
 KW hepatitis D virus; hepatitis E virus.
 XX
 OS Unidentified.
 PN WO200191536-A2.
 XX
 PD 06-DEC-2001.
 XX
 PR 04-JUN-2001; 2001WO-US18238.
 XX
 PR 02-JUN-2000; 2000US-0585599.
 XX
 PR (GENP-) GENPHAR INC.
 XX
 PI Wang D;
 XX
 PN WPI; 2002-122028/16.
 XX
 DR
 PT Replication-incompetent recombinant virus useful as vaccine for
 PT immunizing humans against pathogenic virus, bacteria and parasites, has
 PT antigens heterologous to the virus and an immuno-stimulator sequence
 XX
 PS Example; Page 67; 142pp; English.
 XX
 CC The present invention describes a replication-incompetent recombinant
 CC virus (RV) comprising antigen sequences heterologous to RV, each sequence
 CC encoding a bacterial, viral or parasitic antigen whose expression elicits
 CC an immune response against the antigen and cells expressing the antigen
 CC in a host upon infection of host by RV, and an immuno-stimulator (IS)
 sequence heterologous to RV. The expression of the IS sequence in the

CC host enhances the immunogenicity of the antigen, and RV does not cause a malignancy naturally associated with the pathogen in the host. The RV has
 CC virucide, antibacterial, antiparasitic, protozoacide and anti-HIV, and
 CC can be used in vaccine production. The RV is useful for enhancing the
 CC immunity of a host to one or more pathogenic bacteria such as *Bacillus*
 CC *tuberculosis*, *B. anthracis*, *spirochete*, *Borrelia burgdorferi* that causes
 CC the Lyme disease in animals, parasites such as *malaria*, *Cryptosporidium*,
 CC *Leishmania*, *Histomonias*, *Leucocytozoon*, *Plasmodium*, *Toxoplasma*, *Trichomonas*,
 CC viruses such as HIV type 1 and type 2, influenza virus, respiratory
 CC syncytial virus, herpes simplex virus type 1 and type 2, human papilloma
 CC virus, Ebola virus, Marburg virus and hepatitis A, B, C, D and E virus.
 CC RV induces a strong and long-lasting immune response to various strains
 CC or types of pathogens in the host. The present sequence represents a
 CC glycoprotein cleavage site peptide which is given in the exemplification
 CC of the present invention.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RTR 3
 Db 2 RTR 4

RESULT 15

AAR75674

ID AAR75674 standard; peptide: 6 AA.

XX

AC AAR75674;

XX

DT 12-JAN-1996 (first entry)

XX

DE Streptokinase-binding plasmin B chain peptide.

XX

KW Streptokinase; plasmin B; affinity chromatography; purification;

KW

isolation.

XX

OS Homo sapiens.

XX

PN GB2284422-A.

XX

PD 07-JUN-1995.

XX

PF 29-NOV-1994; 94GB-0024112.

XX

PR 29-NOV-1993; 93GB-0024473.

XX

PA (OXFO-) OXFORD RES SUPPORT CO LTD.

XX

PT Cederholm-Williams SA;

XX

DR WPI; 1995-196178/25.

XX

PT New peptide sequences from Plasmin B chain - able to bind other
 PT proteins esp. Streptokinase, useful for affinity purifcn.

XX

PS Claim 3; Page 6; 14pp; English.

XX

CC AAR75669-R75678 and AAR75682 are streptokinase binding peptides derived
 CC from the human Plasmin B chain in the regions 576-600, 620-640 or
 CC 640-655 amino acids. The peptides are also capable of binding other
 CC proteins useful particularly when immobilised on a solid support for
 CC use in affinity chromatography.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 16; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 1 RTR 3

Search completed: September 9, 2003, 23:31:40
 Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

ON4 protein - protein search, using sw model
Run on: September 9, 2003, 23:34:34 ; Search time 28.125 seconds
(without alignments) 14.646 Million cell updates/sec

Title: US-09-967-003-2
Perfect score: 15
Sequence: 1 RTR 3

Searched: BLOSUM2

Scoring table: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*

1: /cgn2_6/ptodata/1/pubpaa/us07_pubcomb.pep:*

2: /cgn2_6/ptodata/1/pubpaa/pct_new_pub.pep:*

3: /cgn2_6/ptodata/1/pubpaa/us06_pubcomb.pep:*

4: /cgn2_6/ptodata/1/pubpaa/us09_pubcomb.pep:*

5: /cgn2_6/ptodata/1/pubpaa/us07_new_pub.pep:*

6: /cgn2_6/ptodata/1/pubpaa/pcus_pubcomb.pep:*

7: /cgn2_6/ptodata/1/pubpaa/us08_new_pub.pep:*

8: /cgn2_6/ptodata/1/pubpaa/us09_pubcomb.pep:*

9: /cgn2_6/ptodata/1/pubpaa/us06_new_pub.pep:*

10: /cgn2_6/ptodata/1/pubpaa/us09_pubcomb.pep:*

11: /cgn2_6/ptodata/1/pubpaa/us09_new_pub.pep:*

12: /cgn2_6/ptodata/1/pubpaa/us09_pubcomb.pep:*

13: /cgn2_6/ptodata/1/pubpaa/us10_pubcomb.pep:*

14: /cgn2_6/ptodata/1/pubpaa/us10_pubcomb.pep:*

15: /cgn2_6/ptodata/1/pubpaa/us10_pubcomb.pep:*

16: /cgn2_6/ptodata/1/pubpaa/us10_new_pub.pep:*

17: /cgn2_6/ptodata/1/pubpaa/us60_new_pub.pep:*

18: /cgn2_6/ptodata/1/pubpaa/us60_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
US-09-967-003-2
Sequence 2, Application US/09967003
Patent No. US20020107202A1
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
Fister, Robert
APPLICANT: Blalock, James
APPLICANT: Matteo, Villain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC FILE REFERENCE: 92705/57
CURRENT APPLICATION NUMBER: US/09/967,003
PRIOR APPLICATION NUMBER: US/09/521,365
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1993-03-08
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0

SEQ ID NO 2
LENGTH: 3
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid sequence 7, Appli
OTHER INFORMATION: sequence 7, Appli
OTHER INFORMATION: sequence 3, Appli
OTHER INFORMATION: sequence 10, Appli
SEQUENCE 4, Appli
SEQUENCE 8, Appli
SEQUENCE 54, Appli
SEQUENCE 78, Appli
SEQUENCE 68, Appli
SEQUENCE 11, Appli
SEQUENCE 78, Appli
SEQUENCE 77, Appli
SEQUENCE 17, Appli

SEQUENCE 8, Appli
SEQUENCE 90, Appli
SEQUENCE 3182, Appli
SEQUENCE 28, Appli
SEQUENCE 464, Appli
SEQUENCE 37, Appli
SEQUENCE 13, Appli
SEQUENCE 16, Appli
SEQUENCE 23, Appli
SEQUENCE 31, Appli
SEQUENCE 34, Appli
SEQUENCE 40, Appli
SEQUENCE 130, Appli
SEQUENCE 158, Appli
SEQUENCE 247, Appli
SEQUENCE 331, Appli
SEQUENCE 349, Appli
SEQUENCE 361, Appli
SEQUENCE 438, Appli
SEQUENCE 443, Appli
SEQUENCE 444, Appli
SEQUENCE 446, Appli
SEQUENCE 455, Appli
SEQUENCE 457, Appli
SEQUENCE 462, Appli
SEQUENCE 524, Appli
SEQUENCE 530, Appli
SEQUENCE 536, Appli

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	3	10 US-09-967-003-2 Sequence 2, Appli
2	15	100.0	4	10 US-09-967-003-2 Sequence 7, Appli
3	15	100.0	5	10 US-09-967-003-3 Sequence 3, Appli
4	15	100.0	5	10 US-09-967-003-3 Sequence 10, Appli
5	15	100.0	5	12 US-10-003-05-10 Sequence 4, Appli
6	15	100.0	5	14 US-10-003-05-10 Sequence 4, Appli
7	15	100.0	5	15 US-10-212-634-4 Sequence 8, Appli
8	15	100.0	6	10 US-09-800-33-8 Sequence 7, Appli
9	15	100.0	6	10 US-09-954-637-54 Sequence 54, Appli
10	15	100.0	6	10 US-09-950-62-78 Sequence 78, Appli
11	15	100.0	6	10 US-09-837-07-68 Sequence 68, Appli
12	15	100.0	6	10 US-09-881-572A-11 Sequence 11, Appli
13	15	100.0	6	11 US-09-858-852A-77 Sequence 78, Appli
14	15	100.0	6	11 US-09-500-700-17 Sequence 77, Appli
15	100.0	6	11 US-10-059-749-17 Sequence 17, Appli	

RESULT 2
US-09-936-960-7
Sequence 7, Application US/09736960
PATENT NO. US20020102267A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
TITLE OF INVENTION: CLASP-5 Transmembrane Protein
FILE REFERENCE: 020054-00051IUS
CURRENT APPLICATION NUMBER: US/09/7736,960
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US/09/7736,960
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 09/547,276
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,460
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 09/687,837
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,503
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,508
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,539
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/240,543
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 7
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:CLASP-5 homolog
OTHER INFORMATION: of furin protease consensus cleavage sequence

US-09-936-960-7
Query Match 100.0%; Score 15; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTR 3
Db 2 RTR 4

RESULT 3
US-09-800-433-7
Sequence 7, Application US/09800433
PATENT NO. US2002010378A1
GENERAL INFORMATION:
APPLICANT: O'Hare and Elliott
TITLE OF INVENTION: Materials and methods for intracellular transport and
FILE REFERENCE: 49408

RESULT 4
US-09-967-003-3
Sequence 3, Application US/09967003
PATENT NO. US20020107202A1
GENERAL INFORMATION:
APPLICANT: Haddox, Jeffrey
APPLICANT: Pfister, Robert
APPLICANT: Blalock, James
APPLICANT: Matteo, Villain
TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC
FILE REFERENCE: 92750/57
CURRENT APPLICATION NUMBER: US/09/967,003
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/521,365
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,409
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 3
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: description of artificial sequence: amino acid
OTHER INFORMATION: sequence of complementary peptide inhibitor of
US-09-967-003-3
Query Match 100.0%; Score 15; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTR 3
Db 1 RTR 3

RESULT 5
US-10-286-332A-10
Sequence 10, Application US/10286332A
PATENT NO. US20030130459A1
GENERAL INFORMATION:
APPLICANT: Wang, Danier
TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
FILE REFERENCE: 22489-738
CURRENT APPLICATION NUMBER: US/10/286,332A
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 09/585,599

PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: PCIV/US01/18238
 PRIORITY: 2001-06-04
 PRIORITY FILING DATE: 2001-11-01
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Ebola virus
 US-10-286-332A-10

Query Match 100.0%; Score 15; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 RTR 3
 Db 1 RTR 4

RESULT 6
 US-10-003-035-10
 Sequence 10, Application US/10003035
 Publication No. US20020155127A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Danher
 TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
 FILE REFERENCE: 22488-712
 CURRENT APPLICATION NUMBER: US/10/003, 035
 CURRENT FILING DATE: 2001-11-01
 PRIOR APPLICATION NUMBER: 09/585, 599
 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: PCT/US01/18238
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Ebola virus
 US-10-003-035-10

Query Match 100.0%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 RTR 3
 Db 1 RTR 4

RESULT 7
 US-10-212-634-4
 Sequence 4, Application US/10212634
 Publication No. US/20030119770A1
 GENERAL INFORMATION:
 APPLICANT: La, Zhenan
 APPLICANT: Reiser, Jukob
 APPLICANT: Brady, Roscoe O.
 TITLE OF INVENTION: INTERCELLULAR DELIVERY OF A HERPES
 TITLE OF INVENTION: SIMPLEX VIRUS VP22 FUSION PROTEIN FROM CELLS INFECTED WITH
 FILE REFERENCE: NIH207.001A
 CURRENT APPLICATION NUMBER: US/10/212, 634
 CURRENT FILING DATE: 2002-08-02
 PRIOR APPLICATION NUMBER: US 60/310, 012
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 5

Query Match 100.0%; Score 15; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 RTR 3
 Db 1 RTR 3

RESULT 8
 US-09-800-433-8
 Sequence 8, Application US/09800433
 Patent No. US20020106378A1
 GENERAL INFORMATION:
 APPLICANT: O'Hare and Elliott
 TITLE OF INVENTION: Materials and methods for intracellular transport and
 FILE REFERENCE: 49408
 CURRENT APPLICATION NUMBER: US/09/800, 433
 CURRENT FILING DATE: 2000-03-05
 PRIOR APPLICATION NUMBER: 09/395, 344
 PRIOR FILING DATE: 1999-09-13
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-800-433-8

Query Match 100.0%; Score 15; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 RTR 3
 Db 1 RTR 3

RESULT 9
 US-09-954-697-54
 Sequence 54, Application US/09954697
 Patent No. US/20020106631A1
 GENERAL INFORMATION:
 APPLICANT: Alnemri, Emad S.
 TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSBS
 FILE REFERENCE: 480140-431D2
 CURRENT APPLICATION NUMBER: US/09/954, 697
 CURRENT FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 54
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-954-697-54

Query Match 100.0%; Score 15; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 RTR 3
 Db 1 RTR 3

CURRENT APPLICATION NUMBER: US/09/500,700
 CURRENT FILING DATE: 2003-01-10
 PRIORITY APPLICATION NUMBER: US 08/763,813
 PRIORITY FILING DATE: 1997-05-27
 PRIORITY APPLICATION NUMBER: US 08/676,318
 PRIORITY FILING DATE: 1996-12-30
 PRIORITY APPLICATION NUMBER: PCWUS95/00829
 PRIORITY FILING DATE: 1995-01-18
 PRIORITY APPLICATION NUMBER: US 08/712,604
 PRIORITY FILING DATE: 1994-09-28
 PRIORITY APPLICATION NUMBER: US 08/183,119
 NUMBER OF SEQ ID NOS: 127
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 77
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Modified sequence of finger 1 of zif268
 US-09-500-700-77

Query Match 100.0%; Score 15; DB 11; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy	1 RTR 3
Db	111 4 RTR 6

RESULT 15
 US-10-059-749-17
 Sequence 17, Application US/10059749
 Publication No. US2002018350A1
 GENERAL INFORMATION:
 APPLICANT: Alnemri, Emaad S.
 Fernandes-Alnemri, Teresa
 Littwack, Gerald S.
 TITLE OF INVENTION: Apoptotic Protease Mcb6, Nucleic Acids
 Encoding Same and Methods of Use
 NUMBER OF SEQUENCES: 87
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/059,749
 FILING DATE: 29-Jan-2002
 CLASSIFICATION: <unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/865,579
 FILING DATE: 29-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 2180
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-9849
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-10-059-749-17

TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-10-059-749-17

Query Match 100.0%; Score 15; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 3; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 111
1 RTR 3

Search completed: September 9, 2003, 23:47:27
 Job time : 29.125 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

On protein - protein search, using sw model

Run on:

September 9, 2003, 23:31:48 ; search time 213 seconds

(without alignments) 12.816 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15

Sequence: 1 RTR 3

Scoring table: BLOSUM2

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 9091918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA_Main: *
1: /cgn2_6/ptodata/1/paa/US06_COHP_PEP: *
2: /cgn2_6/ptodata/1/paa/US07_COHP_PEP: *
3: /cgn2_6/ptodata/1/paa/US07_COHP_PEP: *
4: /cgn2_6/ptodata/1/paa/US080_COHP_PEP: *
5: /cgn2_6/ptodata/1/paa/US081_COHP_PEP: *
6: /cgn2_6/ptodata/1/paa/US082_COHP_PEP: *
7: /cgn2_6/ptodata/1/paa/US083_COHP_PEP: *
8: /cgn2_6/ptodata/1/paa/US084_COHP_PEP: *
9: /cgn2_6/ptodata/1/paa/US085_COHP_PEP: *
10: /cgn2_6/ptodata/1/paa/US086_COHP_PEP: *
11: /cgn2_6/ptodata/1/paa/US087_COHP_PEP: *
12: /cgn2_6/ptodata/1/paa/US088_COHP_PEP: *
13: /cgn2_6/ptodata/1/paa/US089_COHP_PEP: *
14: /cgn2_6/ptodata/1/paa/US090_COHP_PEP: *
15: /cgn2_6/ptodata/1/paa/US091_COHP_PEP: *
16: /cgn2_6/ptodata/1/paa/US092_COHP_PEP: *
17: /cgn2_6/ptodata/1/paa/US093_COHP_PEP: *
18: /cgn2_6/ptodata/1/paa/US094_COHP_PEP: *
19: /cgn2_6/ptodata/1/paa/US095_COHP_PEP: *
20: /cgn2_6/ptodata/1/paa/US096_COHP_PEP: *
21: /cgn2_6/ptodata/1/paa/US097_COHP_PEP: *
22: /cgn2_6/ptodata/1/paa/US098_COHP_PEP: *
23: /cgn2_6/ptodata/1/paa/US099_COHP_PEP: *
24: /cgn2_6/ptodata/1/paa/US099B_COHP_PEP: *
25: /cgn2_6/ptodata/1/paa/US100_COHP_PEP: *
26: /cgn2_6/ptodata/1/paa/US101_COHP_PEP: *
27: /cgn2_6/ptodata/1/paa/US102_COHP_PEP: *
28: /cgn2_6/ptodata/1/paa/US103_COHP_PEP: *
29: /cgn2_6/ptodata/1/paa/US104_COHP_PEP: *
30: /cgn2_6/ptodata/1/paa/US106_COHP_PEP: *
31: /cgn2_6/ptodata/1/paa/US60_COHP_PEP: *
32: /cgn2_6/ptodata/1/paa/US60_COHP_PEP: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	3	PCT-US00-06062-2
				Sequence 2, Appli
				Sequence 3, Appli
				Sequence 4, Appli
				Sequence 5, Appli
				Sequence 6, Appli
				Sequence 7, Appli
				Sequence 8, Appli
				Sequence 9, Appli
				Sequence 10, Appli
				Sequence 11, Appli
				Sequence 12, Appli
				Sequence 13, Appli
				Sequence 14, Appli
				Sequence 15, Appli
				Sequence 16, Appli
				Sequence 17, Appli
				Sequence 18, Appli
				Sequence 19, Appli
				Sequence 20, Appli
				Sequence 21, Appli
				Sequence 22, Appli
				Sequence 23, Appli
				Sequence 24, Appli
				Sequence 25, Appli
				Sequence 26, Appli
				Sequence 27, Appli
				Sequence 28, Appli
				Sequence 29, Appli
				Sequence 30, Appli
				Sequence 31, Appli
				Sequence 32, Appli
				Sequence 33, Appli
				Sequence 34, Appli
				Sequence 35, Appli
				Sequence 36, Appli
				Sequence 37, Appli
				Sequence 38, Appli
				Sequence 39, Appli
				Sequence 40, Appli
				Sequence 41, Appli
				Sequence 42, Appli
				Sequence 43, Appli
				Sequence 44, Appli
				Sequence 45, Appli
				Sequence 46, Appli
				Sequence 47, Appli
				Sequence 48, Appli
				Sequence 49, Appli
				Sequence 50, Appli
				Sequence 51, Appli
				Sequence 52, Appli
				Sequence 53, Appli
				Sequence 54, Appli

ALIGNMENTS

RESULT 1

PCT-US00-06062-2

; Sequence 2, Application PC/TUS0006062

; GENERAL INFORMATION:

APPLICANT: Haddox, Jeffrey Lynn

APPLICANT: Blalock, James Edwin

APPLICANT: Pfister, Roswell Robert

APPLICANT: Villain, Tattee

TITLE OF INVENTION: Synthetic Complementary Peptides and

FILE REFERENCE: D601PCT

CURRENT APPLICATION NUMBER: PCT/TUS00/06062

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: US 60/123,409

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2, LENGTH: 3

TYPE: PRT

ORGANISM: artificial sequence

FEATURE: amino acid sequence of complementary peptide

OTHER INFORMATION: inhibitor of neutrophils; used as monomer

OTHER INFORMATION: dimer and tetramer

PCT-US00-05062-2

Query Match 100.0%; Score 15; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 5.3e+06; Mismatches 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 2

US-09-967-003-2

Sequence 2, Application US/09967003

GENERAL INFORMATION:

APPLICANT: Haddox, Jeffrey

APPLICANT: Pfister, Robert

APPLICANT: Blalock, James

APPLICANT: Matteo, Villain

TITLE OF INVENTION: SYNTHETIC COMPLEMENTARY PEPTIDES AND OPHTHALMOLOGIC

FILE REFERENCE: 92750/57

CURRENT APPLICATION NUMBER: US/09/967,003

CURRENT FILING DATE: 2001-09-28

PRIORITY NUMBER: US/09/521,365

PRIORITY FILING DATE: 2000-03-08

PRIORITY APPLICATION NUMBER: US 60/123,409

SEQUENCE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 3

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: description of artificial sequence: amino acid

OTHER INFORMATION: sequence of complementary peptide inhibitor of

OTHER INFORMATION: used as a monomer, dimer, and tetramer

Query Match 100.0%; Score 15; DB 25; Length 3;
 Best Local Similarity 100.0%; Pred. No. 5.3e+06; Mismatches 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 3

PCT-US97-12974A-61

Sequence 61, Application PC/US9712974A

GENERAL INFORMATION:

APPLICANT: Chang, Conway

APPLICANT: Gu, Leo

APPLICANT: Chen, Jie

TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penile & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/12974A

FILING DATE: 23 Jul 97

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/685,589

FILING DATE: 24-Jul-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30.742

REFERENCE/DOCKET NUMBER: 8057-026-228

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

FILING DATE: 23 Jul 97
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/685,589

FILING DATE: 24-Jul-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30.742

REFERENCE/DOCKET NUMBER: 8057-026-228

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-869-9741

TELEFAX: 212-869-9741

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: "Peptide"

OTHER INFORMATION: /product- "Beta-turn"

PCT-US97-12974A-61

Query Match 100.0%; Score 15; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.3e+06; Mismatches 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 4

PCT-US97-12974A-68

Sequence 68, Application PC/US9712974A

GENERAL INFORMATION:

APPLICANT: Chang, Conway

APPLICANT: Gu, Leo

APPLICANT: Chen, Jie

TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penile & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/12974A

FILING DATE: 23 Jul 97

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/685,589

FILING DATE: 24-Jul-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30.742

REFERENCE/DOCKET NUMBER: 8057-026-228

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide

FEATURE: ;
 NAME/KEY: Peptide
 LOCATION: 1..4
 OTHER INFORMATION: /product= "Beta-turn"

Query Match 100.0%; Score 15; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.3e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0; Gaps 0;

QY 1 RTR 3
 Db 2 RTR 4

RESULT 5
 PCT-US97-19557-61
 ; SEQUENCE 61: Application PC/US9719557
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Conway
 ; APPLICANT: Gu, Leo
 ; APPLICANT: Chen, Jie
 ; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
 ; NUMBER OF SEQUENCES: 241
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Penne & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PC/US97/19557
 ; FILING DATE: herewith
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 8067-048-228
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-9741
 ; TELEFAX: 66141
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide

FEATURE: ;
 NAME/KEY: Peptide
 LOCATION: 1..4
 OTHER INFORMATION: /product= "Beta-turn"

Query Match 100.0%; Score 15; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.3e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0; Gaps 0;

QY 1 RTR 3
 Db 2 RTR 4

RESULT 6
 PCT-US97-19557-68
 ; Sequence 68, Application PC/US9719557
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Conway
 ; APPLICANT: Gu, Leo
 ; APPLICANT: Chen, Jie
 ; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
 ; NUMBER OF SEQUENCES: 241
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Penne & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PC/US97/19557
 ; FILING DATE: herewith
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 8067-048-228
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-9741
 ; TELEFAX: 66141
 ; INFORMATION FOR SEQ ID NO: 68:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide

FEATURE: ;
 NAME/KEY: Peptide
 LOCATION: 1..4
 OTHER INFORMATION: /product= "Beta-turn"

Query Match 100.0%; Score 15; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 5.3e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0; Gaps 0;

QY 1 RTR 3
 Db 2 RTR 4

RESULT 7
 US-09-340-852-61
 ; Sequence 61, Application US/09340852
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Conway
 ; APPLICANT: Gu, Leo
 ; APPLICANT: Chen, Jie
 ; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
 ; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
 ; NUMBER OF SEQUENCES: 222
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Penne & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York

QY 1 RTR 3

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 7
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:CLASP-5 homolog
 US-09-736-960-7

Query Match	Score	DB	Length	Matches	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
3; Conservative	100.0%	21	4	0;	100.0%	5.3e+06	0;	0	0;

Qy 1 RTR 3
 Db 2 RTR 4

RESULT 10
 US-10-031-289-1758
 Sequence 158, Application US/10031289
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: MASIGNANI Vega
 APPLICANT: SCARLATO Vincenzo
 APPLICANT: SCARSELLI Maria
 APPLICANT: GALEOTTI Cesira
 TITLE OF INVENTION: ANTIIGENIC MENINGOCOCCAL PEPTIDES
 FILE REFERENCE: P022260W0
 CURRENT APPLICATION NUMBER: US-10-031, 289
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: GB-9916529.2
 PRIOR FILING DATE: 1999-07-14
 NUMBER OF SEQ ID NOS: 1769
 SOFTWARE: SeqWin99, version 1.02
 SEQ ID NO: 1758
 LENGTH: 4

Qy 1 RTR 3
 TYPE: PRT
 ORGANISM: Neisseria meningitidis
 US-10-031-289-1758

Query Match	Score	DB	Length	Matches	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
3; Conservative	100.0%	15	4	0;	100.0%	5.3e+06	0;	0	0;

Qy 1 RTR 3
 Db 2 RTR 4

RESULT 11
 PCT-US00-06062-3
 Sequence 3, Application PC/PTUS0006062
 GENERAL INFORMATION:
 APPLICANT: Haddox, Jeffrey Lynn
 APPLICANT: Bialock, James Edwin
 APPLICANT: Pfister, Roswell Robert
 APPLICANT: Villain, Matteo
 TITLE OF INVENTION: Synthetic Complementary Peptides and
 FILE REFERENCE: D6201PCT
 CURRENT APPLICATION NUMBER: PCT/US00/06062
 CURRENT FILING DATE: 2000-03-08
 EARLIER APPLICATION NUMBER: US 60/123,409
 EARLIER FILING DATE: 1999-03-09
 NUMBER OF SEQ ID NOS: 4
 SEQ ID NO: 3
 LENGTH: 5
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: amino acid sequence of complementary peptide

OTHER INFORMATION: inhibitor of neutrophils; used as monomer
 PCT-US00-06062-3
 Query Match

Query Match	Score	DB	Length	Matches	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
3; Conservative	100.0%	1	5	0;	100.0%	5.3e+06	0;	0	0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 12
 PCT-US01-48432-105
 Sequence 105, Application PC/PTUS0148432
 GENERAL INFORMATION:
 APPLICANT: MEDIMMUNE, INC.
 TITLE OF INVENTION: MOLECULES WITH EXTENDED HALF-LIVES, COMPOSITIONS AND USES THE
 FILE REFERENCE: 10271-027-228
 CURRENT APPLICATION NUMBER: PCT/US01/48432
 CURRENT FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: 60/254, 884
 PRIOR FILING DATE: 2000-12-12
 PRIOR APPLICATION NUMBER: 60/238, 760
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 105
 LENGTH: 5

Qy 1 RTR 3
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US01-48432-105

RESULT 13
 PCT-US02-30251-51
 Sequence 51, Application PC/PTUS0230251
 GENERAL INFORMATION:
 APPLICANT: The Government of the United States of America as represented by
 APPLICANT: Secretary, Health and Human Services
 APPLICANT: NABEL, GARY
 APPLICANT: YANG, ZHI-YONG
 APPLICANT: SULLIVAN, NANCY
 APPLICANT: SANCHEZ, ANTHONY
 TITLE OF INVENTION: Development of a Preventive Vaccine for
 TITLE OF INVENTION: Filovirus Infection in Primates
 FILE REFERENCE: NIH221.001PCT
 CURRENT APPLICATION NUMBER: PCT/US02/30251
 CURRENT FILING DATE: 2002-09-24
 PRIOR APPLICATION NUMBER: US 60/336476
 PRIOR FILING DATE: 2001-10-01
 NUMBER OF SEQ ID NOS: 52
 SEQ ID NO: 51
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Ebola Virus
 PCT-US02-30251-51

Query Match

Query Match	Score	DB	Length	Matches	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
3; Conservative	100.0%	1	5	0;	100.0%	5.3e+06	0;	0	0;

Qy 1 RTR 3

Db 2 RTR 4 |||

RESULT 14 PCP-US02-35112-10

; Sequence 10, Application PC/PCPUS0235112

; GENERAL INFORMATION:

; APPLICANT: Wang, Daher

; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS

; FILE REFERENCE: 224486-740

; CURRENT APPLICATION NUMBER: PCP/US02/35112

; PRIORITY FILING DATE: 2002-11-01

; PRIORITY APPLICATION NUMBER: US 09/585, 599

; PRIORITY FILING DATE: 2000-06-02

; PRIORITY APPLICATION NUMBER: PCP/US01/18238

; PRIORITY FILING DATE: 2001-06-04

; PRIORITY APPLICATION NUMBER: US 10/003, 035

; PRIORITY FILING DATE: 2001-11-01

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 10

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Ebola virus

PCP-US02-35112-10

Query Match 100.0%; Score 15; DB 1; Length 5;

Best Local Similarity 100.0%; Pred No. 5.3e+06;

Matches 3; Conservative 0; Mismatch 0;

Indels 0; Gaps 0;

OY 1 RTR 3 |||

Db 2 RTR 4 |||

RESULT 15 US-08-247-572-8

; Sequence 8, Application US/08247572

; GENERAL INFORMATION:

; APPLICANT: Tuomelan, Elaine

; APPLICANT: Masure, Robert

; TITLE OF INVENTION: Antibody Recognizing Endothelial Cell

; TITLE OF INVENTION: Ligand for Leukocyte CR3

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wyatt, Gerber, Burke and Badie

; STREET: 645 Madison Avenue, 5th Floor

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/247,572

; FILING DATE: 23-MAY-1994

; CLASSIFICATION: 424

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US92/03725 PCT

; FILING DATE: 04-MAY-1992

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/695, 613

; FILING DATE: 03-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Burke, Henry T.

; REGISTRATION NUMBER: 18,975

; REFERENCE/DOCKET NUMBER: 18367A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-826-0171

TELEFAX: 212-755-6256 INFORMATION FOR SEQ ID NO: 8;

TELEX: 421733GERRIG SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-247-572-8

Query Match 100.0%; Score 15; DB 6; Length 5;

Best Local Similarity 100.0%; Pred. No. 5.3e+06;

Matches 3; Conservative 0; Mismatch 0;

Indels 0; Gaps 0;

OY 1 RTR 3 |||

Db 2 RTR 4 |||

Search completed: September 9, 2003, 23:45:43

Job time : 215 secs

ORGANISM: UNKNOWN
 FEATURE: OTHER INFORMATION: Class MCH 1 peptides - Influenza nucleoprotein
 US-09-361-107-8

Query Match Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 4 RTR 6

RESULT 3
 US-09-799-250B-16
 Sequence 16, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: Mary Paris
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 16
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 7 RTR 9

RESULT 4
 US-09-799-250B-23
 Sequence 23, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: Mary Paris
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 FILE REFERENCE: 129-34US01 (511582003400)
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 16
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 4 RTR 6

RESULT 5
 US-09-799-250B-31
 Sequence 31, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: Mary Paris
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 31
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 4 RTR 6

RESULT 6
 US-09-799-250B-34
 Sequence 34, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: Mary Paris
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 FILE REFERENCE: 129-34US01 (511582003400)
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 34
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTR 3
 Db 4 RTR 6

RESULT 7
US-09-799-250B-40
Sequence 40, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Farris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09799-250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 40
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-40

Qy	1 RTR 3	111	7 RTR 9						
Query Match	100.0%	Score 15;	DB 5;	Length 9;					
Best Local Similarity	100.0%	Pred. No.	3.9e+04;						
Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

RESULT 8
US-09-799-250B-130
Sequence 130, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Farris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09799-250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 130
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-130

Qy	1 RTR 3	111	7 RTR 9						
Query Match	100.0%	Score 15;	DB 5;	Length 9;					
Best Local Similarity	100.0%	Pred. No.	3.9e+04;						
Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

RESULT 9
US-09-799-250B-158
Sequence 158, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Farris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09799-250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 158
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-158

Qy	1 RTR 3	111	7 RTR 9						
Query Match	100.0%	Score 15;	DB 5;	Length 9;					
Best Local Similarity	100.0%	Pred. No.	3.9e+04;						
Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

RESULT 10
US-09-799-250B-247
Sequence 247, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Farris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT APPLICATION NUMBER: US/09799-250B
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 247
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250B-247

Qy	1 RTR 3	111	7 RTR 9						
Query Match	100.0%	Score 15;	DB 5;	Length 9;					
Best Local Similarity	100.0%	Pred. No.	3.9e+04;						
Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

RESULT 11
US-09-799-250B-331
Sequence 331, Application US/09799250B
GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Farris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)

CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 331
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-799-250B-331

Query Match 100.0%; Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 4 RTR 6

RESULT 12
 US-09-799-250B-349
 Sequence 349, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: MARY PARIS
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 FILE REFERENCE: 129.34US01 (511582003400)
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 349
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-799-250B-349

Query Match 100.0%; Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 7 RTR 9

RESULT 13
 US-09-799-250B-361
 Sequence 361, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: MARY PARIS
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 FILE REFERENCE: 129.34US01 (511582003400)
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 361
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-799-250B-361

Query Match 100.0%; Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 1 RTR 3

RESULT 14
 US-09-799-250B-438
 Sequence 438, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: MARY PARIS
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 FILE REFERENCE: 129.34US01 (511582003400)
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 438
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-799-250B-438

Query Match 100.0%; Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3
 Db 6 RTR 8

RESULT 15
 US-09-799-250B-443
 Sequence 443, Application US/09799250B
 GENERAL INFORMATION:
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Rene S. Hubert
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Arthur B. Raitano
 APPLICANT: MARY PARIS
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 121PIFL: A TISSUE SPECIFIC PROTEIN
 FILE REFERENCE: 129.34US01 (511582003400)
 CURRENT APPLICATION NUMBER: US/09/799,250B
 CURRENT FILING DATE: 2003-07-14
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 443
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-799-250B-443

Query Match 100.0%; Score 15; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
111
DB 2 RTR 4

Search completed: September 9, 2003, 23:46:05
Job time : 6.375 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: September 9, 2003, 23:28:28 ; search time 18.75 seconds

Title: US-09-967-003-2

Perfect score: 15
Sequence: 1 RTR 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

1: PIR_76:*

2: pirl1:*

3: pirl2:*

4: pirl3:*

5: pirl4:*

Pred. No. 1s is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

Qy	1 RTR 3	Db	8 RTR 10
----	---------	----	----------

RESULT 1

A20497
neurotensin-related protein - turkey (fragment)

C:Species: *Meleagris gallopavo* (common turkey)

C:Accession: A20497

R.C.Carraway, R.E.; Cochrane, D.E.; Ruane, S.E.

J. Biol. Chem. 262, 15886-15889, 1987

A:Title: Isolation, structures, and biologic activity of neurotensin-related peptide

A:Reference number: A20497; MUID:8058942; PMID:2445741

A:Molecule type: protein

A:Residues: 1-15 <CAR>

C:Superfamily: collagen alpha 3(VI) chain; animal Kunitz-type proteinase inhibitor h

C:Keywords: neuropeptide

Query Match Similarity 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

Qy	1 RTR 3	Db	8 RTR 10
----	---------	----	----------

RESULT 2

PC4385

GCN4L protein homolog - *Pseudomonas* sp. (fragment)

N:Alternate names: molecular chaperone

C:Species: *Pseudomonas* sp.

C:Accession: 06-Nov-1997 #sequence_revision 06-Nov-1997 #text_change 07-May-1999

C:Accession: PC4385

R.Tokunaga, M.; Matsushita, K.; Tokunaga, H.

Biosci. Biotechnol. Biochem. 61, 1388-1390, 1997

A:Title: Identification and NH2-terminal amino acid sequences of DnaK and GroEL homologs

A:Reference number: PC4383; MUID:97446535; PMID:9301123

A:Accession: PC4385

A:Molecule type: protein

A:Residues: 1-20 <TOK>

A:Experimental source: strain 21-Na

C:Comment: This protein plays a role in protein folding.

Query Match Similarity 100.0%; Score 15; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.4e+2; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RTR 3	Db	12 RTR 14
----	---------	----	-----------

1: RTR 3

2: RTR 10

3: RTR 14

4: RTR 10

5: RTR 10

6: RTR 10

7: RTR 10

8: RTR 10

9: RTR 10

10: RTR 10

11: RTR 10

12: RTR 10

13: RTR 10

14: RTR 10

15: RTR 10

16: RTR 10

17: RTR 10

18: RTR 10

19: RTR 10

20: RTR 10

21: RTR 10

22: RTR 10

23: RTR 10

24: RTR 10

25: RTR 10

26: RTR 10

27: RTR 10

28: RTR 10

29: RTR 10

30: RTR 10

31: RTR 10

32: RTR 10

33: RTR 10

34: RTR 10

35: RTR 10

36: RTR 10

37: RTR 10

38: RTR 10

39: RTR 10

40: RTR 10

41: RTR 10

42: RTR 10

43: RTR 10

44: RTR 10

45: RTR 10

46: RTR 10

47: RTR 10

48: RTR 10

49: RTR 10

50: RTR 10

51: RTR 10

52: RTR 10

53: RTR 10

54: RTR 10

55: RTR 10

56: RTR 10

57: RTR 10

58: RTR 10

59: RTR 10

60: RTR 10

61: RTR 10

62: RTR 10

63: RTR 10

64: RTR 10

65: RTR 10

66: RTR 10

67: RTR 10

68: RTR 10

69: RTR 10

70: RTR 10

71: RTR 10

72: RTR 10

73: RTR 10

74: RTR 10

75: RTR 10

76: RTR 10

77: RTR 10

78: RTR 10

79: RTR 10

80: RTR 10

81: RTR 10

82: RTR 10

83: RTR 10

84: RTR 10

85: RTR 10

86: RTR 10

87: RTR 10

88: RTR 10

89: RTR 10

90: RTR 10

91: RTR 10

92: RTR 10

93: RTR 10

94: RTR 10

95: RTR 10

96: RTR 10

97: RTR 10

98: RTR 10

99: RTR 10

100: RTR 10

PC4386 GroEL protein homolog - *Acinetobacter* sp. (fragment)
 N; Alternate names: molecular chaperone
 C; Species: *Acinetobacter* sp.
 C; Date: 06-Nov-1997 #text_change 07-May-1999
 C; Accession: PC4386
 N; Tokunaga, M.; Matsuoka, K.; Tokunaga, H.; 1997
 Biocat. Biotechnol. Biochem. 61, 1388-1390, 1997
 A; Title: Identification and N-terminal amino acid sequences of Dnak and GroEL homologs
 A; Reference number: PC4383; MUID:9744635; PMID:9301123
 A; Accession: PC4386
 A; Molecule type: protein
 A; Residues: 1-20 <TOK>
 A; Experimental source: strain 204-1
 C; Comment: This protein plays a role in protein folding.

Query Match 100.0%; Score 15; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 3.4e+02; Gaps 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 DB 12 RTR 14

RESULT 4

PR0070 hypothetical protein (gtfc 3' region) - *Streptococcus mutans* (fragment)
 C; Species: *Streptococcus mutans* (man)
 C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 18-Jun-1993
 C; Accession: PR0070
 R; Ueda, S.; Shioza, T.; Kuramitsu, H.K.
 Gene 69, 101-109, 1988
 A; Title: Sequence analysis of the gtfc gene from *Streptococcus mutans* GS-5.
 A; Reference number: JN0345; MUID:9313980; PMID:2976010
 A; Accession: PR0070
 A; Molecule type: DNA
 A; Residues: 1-22 <OED>
 A; Experimental source: strain GS-5

Query Match 100.0%; Score 15; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. NO. 3.7e+02; Gaps 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 DB 13 RTR 15

RESULT 5

S33594 cystic fibrosis transmembrane conductance regulator - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
 C; Accession: S33594
 R; Mello, C.A.; Serra, C.; Stoyanova, V.; Aguzzoli, C.; Faraguna, D.; Tamanini, A.; Burton
 FEBS Lett. 325, 159-162, 1993
 A; Title: Alternative splicing of a previously unidentified CFTTR exon introduces an in-frame deletion in the CFTTR gene
 A; Reference number: S33593; MUID:9335904; PMID:7689062
 A; Accession: S33594
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-25 <HEL>
 A; Cross-references: GB:S64699; NID:9408285; PIDN:AAB27879.1; PID:9408286
 A; Cross-references: M3:9408285; PIDN:9408285; PID:9408286
 A; Cross-references: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 15; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. NO. 3.9e+02; Gaps 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 DB 6 RTR 8

RESULT 6

R6B4B ribosomal protein L41-e, cytosolic - yeast (*Saccharomyces cerevisiae*)
 N; Alternate names: protein D290; protein YDL133c-a; protein YDL184c; ribosomal protein
 C; Species: *Saccharomyces cerevisiae*
 C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 01-Sep-2000
 C; Accession: S22246; S22247; S11264; S58733; S67739; S78073
 R; Suzuki, K.; Hashimoto, T.; Otaka, E.
 Curr. Genet. 17, 185-190, 1990
 A; Title: Yeast ribosomal proteins XI. Molecular analysis of two genes encoding YL41-e
 A; Reference number: S22246; MUID:90254826; PMID:2187623
 A; Accession: S22246
 A; Molecule type: DNA
 A; Residues: 1-25 <SUV>
 A; Cross-references: EMBL:X16065; GSPDB:GN0004; MIPS:YDL184c; NID:94817; PIDN:CNA342C
 A; Genetics: RPL7B
 A; Accession: S22247
 A; Molecule type: DNA
 A; Residues: 1-25 <SUV>
 A; Cross-references: EMBL:X16065; GSPDB:GN0004; MIPS:YDL184c; NID:94817; PIDN:CNA342C
 A; Genetics: RPL7A
 R; Okada, E.; Higo, K.I.; Itoh, T.
 Mol. Gen. Genet. 195, 544-546, 1984
 A; Title: Yeast ribosomal proteins. VIII. Isolation of two proteins and sequence chara
 A; Reference number: S11249
 A; Accession: S11264
 A; Molecule type: protein
 A; Residues: 1-25 <OMA>
 R; Verhasselt, P.; Voet, M.; Volckaert, G.
 Yeast 11, 961-966, 1995
 A; Title: New open reading frames, one of which is similar to the nifV gene of Azotobac
 A; Reference number: S58730; MUID:96021607; PMID:8533471
 A; Accession: S58733
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-25 <VERB>
 A; Cross-references: EMBL:X83276; NID:91004294; PIDN:CAA58262.1; PID:91004310
 A; Genetics: RPL47A
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
 A; Reference number: S67735
 A; Accession: S67739
 A; Molecule type: DNA
 A; Residues: 1-25 <VOR>
 A; Cross-references: EMBL:Z74332; GSPDB:GN0004; MIPS:YDL184c; NID:91431298; PIDN:CNA9
 A; Experimental source: strain S28BC
 A; Genetics: RPL47A
 R; Saluz, H.P.; Woelfl, S.; Hanemann, V.
 submitted to the Protein Sequence Database, July 1996
 A; Reference number: S67677
 A; Accession: S78073
 A; Molecule type: DNA
 A; Residues: 1-25 <SAE>
 A; Cross-references: EMBL:Z74181; NID:91431202; PIDN:CAA98705.1; PID:91903289; GSPDB:G
 A; Genetics: RPL47B
 A; Cross-references: MIPS:YDL184c; SGD:S0002343
 A; Gene: SGD:RPL47B
 A; Cross-references: MIPS:YDL133c-a; SGD:S0002293
 A; Map position: 4L
 A; Map position: 4L
 A; Genetics: <RPL47A>
 A; Gene: SGD:RPL47A; YL41A; MIPS:YDL184c
 A; Cross-references: MIPS:YDL184c; SGD:S0002343
 A; Map position: 4L
 C; Superfamily: rat ribosomal protein L41
 C; Keywords: protein biosynthesis; ribosome
 F; 1-25/product: ribosomal protein L41.e #status experimental <MAT>
 Query Match 100.0%; Score 15; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. NO. 4.2e+02; Gaps 0; Mismatches 0; Indels 0; Gaps 0;

QY 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RTR 3	RESULT 9
Db	9 RTR 11	151989
		streptomyycin 3 - Escherichia coli (fragment)
		C;Species: Escherichia coli
		C;Species: Streptomyces
		C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 03-Jun-2002
		C;Accession: 564715
		R;Chan, D.C.; Bedford, M.T.; Leder, P.
		EMBO J. 15, 1045-1054, 1996
		A;Title: Formin binding proteins bear WWP/NW domains that bind proline-rich peptides and
		A;Reference number: 564711; PMID:96183189; PMID:8605874
		A;Accession: 564715
		A;Status: preliminary; nucleic acid sequence not shown
		A;Molecule type: mRNA
		A;Superfamily: formin binding protein; NW repeat homology (fragment) <NW1>
		A;Cross-references: EMBL:047048; NID:gi1255026; PIDN: AAC52476.1; PID:gi1255027
		F; 1-26/Domain: NW repeat homology (fragment) <NW1>
Qy	1 RTR 3	Query Match 100.0%; Score 15; DB 2; Length 26;
Db	17 RTR 19	Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RTR 3	Query Match 100.0%; Score 15; DB 2; Length 27;
Db	22 RTR 24	Best Local Similarity 100.0%; Pred. No. 4.5e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RTR 3	RESULT 10
Db	22 RTR 24	T34643
		hypothetical protein SC10H5.05 SC10H5.05 - Streptomyces coelicolor
		C;Species: Streptomyces coelicolor
		C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
		C;Accession: T34643
		R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
		submitted to the EMBL Data Library, August 1998
		A;Reference number: 221550
		A;Accession: T34643
		A;Status: Preliminary; translated from GB/EMBL/DDBJ
		A;Molecule type: DNA
		A;Residues: 1-29 <OL1>
		A;Cross-references: EMBL:AL031232; PIDN:CAN20277.1; GSDB:GN00070; SCOEDB:SC10H5.05
		A;Experimental source: strain A3(2)
		C;Genetics:
		A;Gene: SCOEDB:SC10H5.05
Qy	1 RTR 3	Query Match 100.0%; Score 15; DB 2; Length 29;
Db	22 RTR 24	Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 RTR 3	RESULT 11
Db	22 RTR 24	CLHY2
		protamine VII - Pacific herring
		N;Alternate names: clupeine
		C;Species: Clupea pallasi, clupea harengus pallasi (pacific herring)
		C;Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
		C;Accession: A38052; A02677
		R; Suzuki, K.; Ando, T.
		J. Biochem. 72, 1419-1432, 1972
		A;Title: Studies on protamines. XVI. The complete amino acid sequence of clupeine VII.
		A;Reference number: A38052; PMID:73223106; PMID:4664740
		A;Accession: A38052
		A;Molecule type: protein
		A;Residues: 1-30 <SPZ>
		C;Superfamily: protamine VII
		C;Keywords: chromosomal protein; DNA binding; spermatogenesis
Qy	1 RTR 3	Query Match 100.0%; Score 15; DB 1; Length 30;
Db	6 RTR 8	

Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTR 3 Db 4 RTR 6

RESULT 12

CLNR2A
protamine YII - Atlantic herring
N;Alternate names: clupeine
C;Species: Clupea harengus, Clupea harengus harengus (Atlantic herring)
C;Accession: A37575, A2677
R;Chang, W.J.; Nukushina, M.; Ishii, S.; Nakahara, C.; Ando, T.
A;Reference number: A37575
A;Accession: A37575
A;Molecule type: protein
A;Residues: 1-30 <RHA>
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 100.0%; Score 15; DB 1; Length 30; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTR 3 Db 4 RTR 6

RESULT 13

152254
gene CYP1B2 protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Accession: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Mar-1999
R;Mukai, K.; Imai, M.; Shimada, H.; Okada, Y.; Ogishima, T.; Ishimura, Y.
B;Biophys. Res. Commun. 180, 1187-1193, 1991
A;Title: Structural differences in 5'-flanking regions of rat cytochrome P-450aldo and P-450c11a
A;Reference number: 152254; MUID:92062142; PMID:1953771
A;Accession: 152254
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-30 <RES>
A;Cross-references: GB:S63898; NID:9238626
A;Genetics:
C;Gene: CYP1B2
C;Superfamily: human cytochrome P450 CYP1B1; cytochrome P450 homology
C;Keywords: heme; transmembrane protein

Query Match 100.0%; Score 15; DB 2; Length 30; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTR 3 Db 20 RTR 22

RESULT 14

548114
cystic fibrosis transmembrane conductance regulator - mouse
C;Species: Mus musculus (house mouse)
C;Accession: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 07-May-1999
R;Tezise, A. E. O.; Buchwald, M.; Higgins, C. F.
Hum. Mol. Genet. 2, 801-802, 1993.
A;Title: Testis-specific, alternative splicing of rodent CFTR mRNA.
A;Reference number: S48114; MUID:9335775; PMID:7689012
A;Accession: S48114

Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Searched: 127863 seqs, 47026705 residues							
Total number of hits satisfying chosen parameters: 127863							
Minimum DB seq length: 0							
Maximum DB seq length: 200000000							
post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries							
Database : Swissprot_41;*							
Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query	Length	DB ID	Description		
1	15	100.0	25	1 RLA1_YEAST	P05746	saccharomyces	34
2	15	100.0	26	1 RSHX_THETH	P32193	thermus thet	35
3	15	100.0	30	1 PRT1_CLUPA	P02235	clupea palli	36
4	15	100.0	32	1 PRT1_ORLVA	Q91185	oryzias lat	37
5	15	100.0	32	1 RAT1_SIVM2	P05912	simian immun	38
6	15	100.0	33	1 Y50A_MYCTU	Q9cb56	mycobacteri	39
7	15	100.0	34	1 PRT1_DICTAU	Q98277	dicentrae	40
8	15	100.0	34	1 PRT1_PERPV	P29629	perca flave	41
9	15	100.0	37	1 RHOX_RHOOP	P22658	rhodococcus	42
10	15	100.0	39	1 NPF_HELAS	P41321	helix asper	43
11	15	100.0	40	1 RBD2_BOVIN	P46160	bos taurus	44
12	15	100.0	42	1 RBD6_BOVIN	P46164	bos taurus	45
13	15	100.0	44	1 RLU34_BRUME	P084dal	brucella me	46
14	15	100.0	44	1 RLU34_LISHO	Q926q3	listeria mo	47
15	15	100.0	45	1 RLU34_CHIRN	Q92601	chlamydia p	48
16	15	100.0	45	1 RLU34_MICLU	P21153	micrococcus	49
17	15	100.0	45	1 RLU34_STREB1	P22820	streptomyce	50
18	15	100.0	45	1 RLU34_STRECO	P27901	streptomyce	51
19	15	100.0	47	1 RLU34_BUCIA1	P57129	buchnera ap	52
20	15	100.0	47	1 RLU34_BUCAR	P29337	buchnera ap	53
21	15	100.0	47	1 RLU34_BUCP	Q89bb35	buchnera ap	54
22	15	100.0	47	1 RLU34_MYCBL	P46386	mycobacteri	55
23	15	100.0	47	1 RLU34_MICPA	Q91718	mycobacteri	56
24	15	100.0	47	1 RLU34_MYCBA	P49229	mycobacteri	57
25	15	100.0	47	1 RLU34_MYCCT	P52829	mycobacteri	58
26	15	100.0	52	1 RLU34_TREPA	Q82210	treponema p	59
27	15	100.0	54	1 BVCB_NPYAC	P05645	autographa	60
28	15	100.0	56	1 HSP_COTJA	P1402	coturnix co	61
29	15	100.0	56	1 Y04B_BOVIN	P51077	borrelia bu	62
30	15	100.0	57	1 BD03_BOVIN	P46161	bos taurus	63
31	15	100.0	58	1 AXP1_ANTRAF	P81548	anthophleura	64
32	15	100.0	59	1 CEC_EBOMMO	P48821	bombyx mori	65
33	15	100.0	59	1 RLU32_BORBU	Q51646	borrelia bu	66

Copyright (c) 1993 - 2003 Compugen Ltd.

Om protein - protein search, using sw model

Run on: September 9, 2003, 23:21:23 ; Search time 10.5 seconds

{without alignments) 13.436 Million cell updates/sec

Title: US-09-967-003-2

Perfect score: 15

Sequence: 1 RTR 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Swissprot_41;*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

ID	RLA1_YEAST	STANDARD:	PRT:	Description
PO5746:			25 AA.	
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	60S ribosomal protein L41 (Y417) (Rel. 37, Last annotation update)			
GN	(RLA1A OR RPL47A OR Y141A OR YDL184C OR D1290) AND (RLA1B OR RPL41B OR Y141B OR YDL133BC)			
GN	Saccharomyces cerevisiae (Baker's yeast); Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyctales; Saccharomyctaceae; Saccharomyces; NEBL ("MaxID=4932"; RN [1])			
RA	SEQUENCE FROM N.A. (RPL41A AND RPL41B).			
RA	MEDLINE=90254826; PubMed=218763;			
RA	Suzuki K., Hashimoto T., Otaka E.; "Yeast ribosomal proteins: XI. Molecular analysis of two genes encoding Y41, an extremely small and basic ribosomal protein, from Saccharomyces cerevisiae.", Curr. Genet. 17:185-190(1990).			
RL	SEQUENCE FROM N.A. (RPL41A).			
RL	RESTRAIN-S288C / FY1679; MEDLINE=956021607; PubMed=8533471;			
RL	Verhasselt P., Voet M., Volckaert G.; "New open reading frames, one of which is similar to the nifV gene of Azotobacter vinelandii, found on a 12.5 kbp fragment of chromosome IV of Saccharomyces cerevisiae.", Yeast 11:961-966(1995).			
RL	RESTRAIN-S288C / FY1679;			
RL	RESTRAIN-S288C / FY1679;			
RL	Woolfl S., Haneman V., Saluz H.P.; "Analysis of a 26.756 bp segment from the left arm of yeast chromosome IV"; Yeast 12:1549-1554(1996).			
RL	SEQUENCE FROM N.A. (RPL41B).			
RL	RESTRAIN-S288C / FY1679;			
RL	RESTRAIN-S288C / FY1679;			
RL	Otaka E., Higo K.-I., Itoh T.; "Yeast ribosomal proteins VIII. Isolation of two proteins and sequence characterization of twenty-four proteins from cytoplasmic ribosomes"; Mol. Gen. Genet. 195:544-546(1984).			
RL	CC - MISCELLANEOUS: THERE ARE TWO GENES FOR L41 IN YEAST.			
RL	CC - SIMILARITY: BELONGS TO THE L41E FAMILY OF RIBOSOMAL PROTEINS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			

ALIGMENTS

P17138 helobdella

P04139 pseudomonas

P03768 bacteriophaga

P41699 autographa

P15340 gallus gallus

083785 treponema p

P15482 streptomyce

P24835 synchocystis

P24649 bombyx mori

0926r8 chlamydia p

Q8kam8 chlorobium

CC	RC
DR	DR
EMBL: X116065; CAA24201; 1;	EMBL: MEDLINE-2109773; PubMed-11163189;
DR	DR
EMBL: X116066; CAA24202; 1;	Brodersen D.E., Clemons W.M. Jr., Carter A.P., Morgan-Warren R.J.,
DR	RA
EMBL: X83216; CAA5262; 1; -;	Wimberly B.T., Ramakrishnan V.
DR	RT
EMBL: Z74232; CAA88759; 1; -;	*The structural basis for the action of the antibiotics tetracycline, pactamycin, and hydromycin B on the 30S ribosomal subunit.**;
DR	RT
EMBL: Z74181; CAA89705; 1; -;	Cell 1103:1143-1154 (2000).
DR	RL
EMBL: X96876; CAA55626; 1; -;	RN [6]
DR	RR
PTR: S22466; R6BYR;	X-RAY CRYSTALLOGRAPHY (3.00 ANGSTROMS) OF THE 30S SUBUNIT.
DR	RC
SGD: S002343; RPL41A.	SPECIES-T: thermophilus;
DR	RX
PRAM; PRP0162; Ribosomal 141; 1.	MEDLINE-20466111; PubMed-11014183;
KW	RC
Ribosomal protein; Multigene family.	Carter A.P., Clemons W.M. Jr., Brodersen
SQ	RA
SEQUENCE 25 AA; 3337 MW; BD2629DD9ED85381 CRC64;	Wimberly B.T., Ramakrishnan V.**Functional insights from the structure of the 30S ribosomal subunit and its interactions with antibiotics.**
OY	RT
1 RTR 3	Nature 407:340-348 (2000).
Db	RL [7]
9 RTR 11	X-RAY CRYSTALLOGRAPHY (5.00 ANGSTROMS) OF THE RIBOSOME.
RESULT 2	SPECIES-T: thermophilus;
RSKX-THETH	MEDLINE-21402420; PubMed-11511350;
ID	RC
RHMX-THETH STANDARD:	Yusupova G.Z., Yusupov M.M., Cate J.H.D., Noller H.F.;
ID	RT
P32193; PR0383; Q92AB;	*The path of messenger RNA through the ribosome.**
DT	RL [8]
01-OCT-1993 (Rel. 27, Created)	Cell 106:233-241 (2001).
DT	RN [8]
01-OCT-1993 (Rel. 27, Last sequence update)	X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF THE 30S SUBUNIT.
DT	RC
28-FEB-2003 (Rel. 41, Last annotation update)	MEDLINE-21192023; PubMed-11296217;
DE	RA
30S ribosomal protein Thx.	Pirotta M., Schlueter F., Hamm J., Zarivach R., Glueckmann M.
GN	RA
RPSU.	Avila H., Bashan A., Bartels H., Auerbach T., Jacobi C., Hartsch T.,
OS	RA
Thermus thermophilus, and	Yonath A., Franceschi F.**Crystals, structures of complexes of the small ribosomal subunit with tetracycline, edeine and I13.**
OC	RT
Bacteria; Deinococcus; Thermus; Deinococci; Thermales; Thermaceae;	EMBO J. 20:1829-1839 (2001).
OC	RL
Thermus.	RN [9]
OX	X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF THE 30S SUBUNIT.
RP	RC
SEQUENCE-TAXID-274, 271;	SPECIES-T: thermophilus;
RN	RT
[1]	MEDLINE-2111954; PubMed-11228145;
RP	RC
SEQUENCE-MEDLINE-9363224; Pubmed-8357533;	Carter A.P., Clemons W.M. Jr., Brodersen
RX	RA
RA	Hartsch T., Wimberly B.T., Ramakrishnan V.**Crystal structure of an initiation factor bound to the 30S ribosomal subunit.**
RC	RT
RC	Science 291:498-501 (2001).
RC	RL [10]
RC	X-RAY CRYSTALLOGRAPHY (5.5 ANGSTROMS) OF THE RIBOSOME.
RX	RC
MEDLINE-95045586; Pubmed-1957245;	SPECIES-T: thermophilus;
RA	RT
RA	MEDLINE-21238753; PubMed-11283358;
RT	RC
thermophilic eubacteria, Thermus thermophilus, T. aquaticus and T. flavius.**	Yusupov M.M., Yusupova G.Z., Beaumon A., Lieberman K., Ernest T.N.,
RT	RA
BIOL. Chem. Hoppe-Seyler 374:377-383 (1993).	Cate J.H.D., Noller H.F.**Crystal structure of the ribosome at 5.5 Å resolution.**
RN	RL
[2]	Science 292:883-896 (2001).
RP	RN [11]
SEQUENCE-T: thermophilus;	X-RAY CRYSTALLOGRAPHY (3.11 ANGSTROMS) OF THE 30S SUBUNIT.
RC	RC
RC	SPECIES-T: thermophilus;
RX	RT
MEDLINE-95045586; Pubmed-1957245;	MEDLINE-21238794; PubMed-11340196;
RA	RA
RA	Ogle J.M., Brodersen D.E., Clemons W.M. Jr., Tarry M.J., Carter A.P.,
RT	RA
RT	Ramakrishnan V.**Recognition of cognate transfer RNA by the 30S ribosomal subunit.**
SEQUENCE FROM N.A. SPECIES-T: thermophilus; STRAIN-HBB / ATCC 27634;	Science 292:897-902 (2001).
RX	RL
MEDLINE-21421773; Pubmed-11530930;	X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
RA	RN
RA	RP
RA	SPECIES-T: thermophilus;
RT	RC
RT	MEDLINE-21238794; PubMed-11340196;
RT	RA
On the characterization of the putative S20-thx operon of Thermus thermophilus;	Ogle J.M., Brodersen D.E., Clemons W.M. Jr., Tarry M.J., Carter A.P.,
RT	RA
RT	Ramakrishnan V.**Recognition of cognate transfer RNA by the 30S ribosomal subunit.**
BIOL. Chem. 382:1001-1006 (2001).	Science 292:897-902 (2001).
RN	RL
[4]	X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
RP	RN [12]
SPECIES-T: thermophilus;	X-RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF THE 30S SUBUNIT.
RX	RC
MEDLINE-20466110; Pubmed-11014182;	SPECIES-T: thermophilus;
RA	RC
Wimberly B.T., Brodersen D.E., Clemons W.M. Jr., Morgan-Warren R.J.,	MEDLINE-21238772; PubMed-11866229;
RA	RA
Carter A.P., Vonrhein C., Harrisch T., Ramakrishnan V.;	Brodersen D.E., Clemons W.M. Jr., Wimberly B.T.,
RT	RA
RT	Ramakrishnan V.**Crystal structure of the 30S ribosomal subunit from Thermus
Structure of the 30S ribosomal subunit.**	thermophilus; structure of the proteins and their interactions with
RL	RT
Nature 407:327-339 (2000).	16S RNA.**
RN	RT
[5]	J. Mol. Biol. 316:725-768 (2002).
X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS) OF THE 30S SUBUNIT.	-1 FUNCTION: Binds at the top of the head of the 30S subunit. It stabilizes a number of different RNA elements and thus is important for subunit structure.
CC	CC
-1 SIMILARITY: BELONGS TO THE S31E FAMILY OF RIBOSOMAL PROTEINS.	CC

DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR TAT protein (Transactivating regulatory protein) (Fragment).
 RN TAT.
 OS Simian immunodeficiency virus (Mm251 isolate) (SIV-MAC).
 OX NCBI_TaxID=11734;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122665; Pubmed=2993293;
 RA Kestler H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
 RA King N.W., Daniel M.D., Desrosiers R.C.;
 RT "Comparison of simian immunodeficiency virus isolates.";
 RL Nature 331:619-622(1988).
 CC [-1] FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 PROMOTER.
 CC -1 SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Nuclear; nucleolar.
 CC -1 MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
 CC
 CC this SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X06879; ; NOT_ANNOTATED_CDS.
 KW HIV; X06879; TATSMW251.
 CC Transcription regulation; Activator; RNA-binding; Nuclear protein;
 CC AIDS.
 FT NON_TER 1 1
 SEQUENCE 32 AA; 3556 MW; 211547CB6F4D817 CRC64;
 CC
 CC Query Match 100.0% Score 15; DB 1; Length 32;
 DR Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 DR Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR
 QY 1 RTR 3
 DR 111
 DB 6 RTR 8
 SQ

RESULT 6

Y50A_MCTU Y50A_MCTU STANDARD; PRT; 33 AA.
 AC QPCB56; ; Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein Rv0500.1/ML2428.1
 GN Rv0500.1 OR Rv0500B OR MT0521.1 OR ML2428.1 OR ML2428A.
 OS Mycobacterium tuberculosis, and
 OC Mycobacterium leprae.
 OC Bacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773, 1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SPECIES=M. tuberculosis; STRAIN=R37Rv;
 MEDLINE=92295987; Pubmed=9634530;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Hornsby T., Jigels K., Krogh A., Molean J., Moulie S., Murphy L.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares R., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX SPECIES=M. tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J., deBoy R., Dodson R., Gwinn M.L., Hart D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolova M.D., Salzberg S.L.,
 Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC [3]
 RP SEQUENCE FROM N.A.
 RX SPECIES=M.leprae; STRAIN=TN;
 RX MEDLINE=21128722; Pubmed=11234002;
 RA Cole S.T., Eiglemeier K., Parkhill J., James K.D., Thomson N.R.,
 Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 Holroyd S., Hornsby T., Jigels K., Lacroix C., Maclean J., Moule S.,
 Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC
 CC this SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; 277162; ; NOT_ANNOTATED_CDS.
 DR EMBL; AE005953; ; NOT_ANNOTATED_CDS.
 DR EMBL; AL5893925; CAC31951; ;
 DR PIR; A67121; A67212;
 DR Leprona; M12420A; ;
 DR TTR; MT0521.1; ;
 DR Tuberculist; Rv0500B; ;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4145 MW; 8156A587F16291F5 CRC64;

Query Match 100.0% Score 15; DB 1; Length 33;
 DR Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 DR Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR
 QY 1 RTR 3
 DR 111
 DB 23 RTR 25

RESULT 7

PRT_DICLIA PRT_DICLIA STANDARD; PRT; 34 AA.
 AC QPS27; ;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR Protamine.
 OS Dicentrarchus labrax (European sea bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopercyigii; Perciformes; Percoidae;
 OC Moronidae; Dicentrarchus.
 OC NCBI_TaxID=13489;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Sperm;

RX	MEDLINE-93139742; PubMed=8421442;
RA	Saperas N., Ribes E., Buesa C., Garcia-Hegart P., Chiva M.;
PRT	"Differences in chromatin condensation during spermiogenesis in two species of fish with distinct protamines.";
RT	J. Exp. Zool. 265:185-194 (1993)
RU	
CC	-!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC	-!- SUBCELLULAR LOCATION: Nuclear.
CC	-!- TISSUE SPECIFICITY: Testis.
KW	Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
SQ	SEQUENCE 34 AA; 4565 MW; EBF41CB25D1F0DE CRC64;
Query Match	100.0%; Score 15; DB 1; Length 34;
OY	Best Local Similarity 100.0%; Pred. No. 1.4e+07; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	16 RTR 18
RESULT 8	
PRT_PPERFV	STANDARD; . PRT; 34 AA.
ID	PRT_PPERFV
AC	P29629; DR 01-ARR-1993 (Rel. 25, Created)
DT	01-ARR-1993 (Rel. 25, Last sequence update)
DR	01-ARR-1993 (Rel. 25, Last annotation update)
DE	protamine.
OS	Perca fluviatilis (Yellow Perch).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Perciformes; Percidae; Percidae; Percidae; Perca.
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Perciformes; Percidae; Percidae; Perca.
OC	NCBI_TaxID=8167;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE-92183928; PubMed=15414489;
RA	Chao H., Davies P.L.;
PRT	"Amino acid sequence of the unique protamine from yellow perch.";
RL	FEMS Lett. 299:166-168 (1992).
CC	-!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC	-!- SUBCELLULAR LOCATION: Nuclear.
CC	-!- TISSUE SPECIFICITY: Testis.
DR	PIR: S204339; S204349.
KW	Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear Protein.
SQ	SEQUENCE 34 AA; 4552 MW; EBF41CB25D2DE CRC64;
Query Match	100.0%; Score 15; DB 1; Length 34;
OY	Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	16 RTR 18
RESULT 9	
HOXF_RHOOP	STANDARD; PRT; 37 AA.
ID	P22558; DR 01-AUG-1991 (Rel. 19, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	NAD-reducing hydrogenase boxS alpha subunit (EC 1.12.1.2) (Fragment).
GN	HOXF
OS	Rhodococcus opacus (Mycobacterium opaca).
OC	Plasmid.
RP	SEQUENCE.
RC	TISSUE=Circumoesophageal ganglion;
RA	MEDLINE-33087780; PubMed=1472263;
RT	Leung P.S., Shaw C., Maule A.G., Thim L., Johnston C.F., Irvine G.B.; "The primary structure of neuropeptide F (NPF) from the garden snail, Helix aspersa.";
RT	Regul. Pept. 41:71-81 (1992).
RL	FUNCTION: MAY HAVE AN IMPORTANT PHYSIOLOGICAL ROLE IN NEUROREGULATION.
CC	-!- SUBCELLULAR LOCATION: Secreted
CC	-!- TISSUE SPECIFICITY: NEURONAL SOMATA AND FIBERS.
CC	-!- SIMILARITY: Belongs to the NPF family.
DR	PIR: A48564; A48564;
DR	InterPro: IPR019555;
DR	pfam: PF00159; hormone3; 1.
SMART	SM00309; PAF_1.
DR	PROSITE: PS0265; PANCREATIC_HORMONE_1; 1.
DR	PROSITE: PS05276; PANCREATIC_HORMONE_2; 1.
KW	Neuropeptide; Amidation.
FT	MOD_RBS 39 39
AMIDATION.	

QY	1	RTR 3	39 AA;	4855 MW;	4B54AA7414CAAE33 CRC64;	OX	NCBI_TaxID=9913;
Query Match	100.0%	Score 15;	DB 1;	Length 39;	Pred. No. 1.6e+02;	RN	[1]
Best Local Similarity	100.0%	Score 15;	DB 1;	Length 39;	Pred. No. 1.6e+02;	RP	SEQUENCE;
Matches	3;	Conservative	0;	Mismatches 0;	Indels 0;	RC	STRAIN="Hereford; TISSUE=Neutrophils;
QY	1	RTR 3	36 RTR 3B		Gaps 0;	RX	MEDLINE-93203265; PubMed-8454635;
RESULT 11						RA	Seisted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
BD02_BOVIN		STANDARD;	PRT;	40 AA.		RA	Smith W., Henschen A.H., Culter J.S.,
ID	BD02_BOVIN		PRT;	40 AA.		RT	"Purification, primary structures, and antibacterial activities of
AC	P46160;					RT	beta-defensins, a new family of antimicrobial peptides from bovine
DT	01-NOV-1995 (Rel. 32, created)					RT	neutrophils";
DT	01-NOV-1995 (Rel. 32, last sequence update)					RL	J. Biol. Chem. 268:641-664B(1993).
DT	16-OCT-2001 (Rel. 40, last annotation update)					CC	-!- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E.COLI ML35
DE	Beta-defensin 2 (BNBD-2) (BNBD-2).					CC	-!- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.
GN	DEFB2.					CC	-!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
OS	Bos taurus (Bovine)					DR	PIR: F45495; F45495.
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	HSSP: P46177; IBBN.
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					DR	InterPro: IPR001855; Defensin_beta.
OX	Bovidae; Bovinae; Bos.					DR	InterPro: IPR0008080; Defensin_beta.
RN	[1]					DR	Pfam: PF0711; Defensin_beta; 1.
RP	SEQUENCE.					DR	SMART: SW00048; DEFSN; 1.
RC	STRAIN=Hereford; TISSUE=Neutrophils;					DR	Antibiotic: Pyrrolidone carboxylic acid.
RX	MEDLINE-93203264; PubMed-8454635;					FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
RA	Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,					FT	DISULFID 9 38 BY SIMILARITY.
RA	Smith W., Henschen A.H., Culter J.S.;					FT	DISULFID 21 31 BY SIMILARITY.
RT	"Purification, primary structures, and antibacterial activities of					FT	DISULFID 21 39 BY SIMILARITY.
RT	beta-defensins, a new family of antimicrobial peptides from bovine					SQ	SEQUENCE 42 AA; 4839 MW; C9E8EB20DREB97 CRC64;
RT	neutrophils";					Query Match	100.0%; Score 15;
RL	J. BIOL. CHEM. 268:641-664B(1993).					Best Local Similarity	100.0%; Pred. No. 1.7e+02;
RA	AND AUREUS 502A.					Matches	3; Conservative 0; Mismatches 0;
RA	AND AUREUS 502A.					Indels	0; Gaps 0;
CC	-!- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES.					RN	
CC	-!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.					QY	1 RTR 3
DR	PIR: C45495; C45495.					Db	24 RTR 26
DR	HSSP: P46170; IBBN.					RESULT 13	
DR	InterPro: IPR001855; Defensin_beta.					RL34_BRUME	STANDARD;
DR	InterPro: IPR006080; Defensin_mammal.					ID	RL34_BRUME STANDARD;
DR	InterPro: IPR00711; Defensin_beta; 1.					AC	Q8TDAL;
DR	SMART; SW00048; DEFSN; 1.					DT	28-FEB-2003 (Rel. 41, Created)
KW	antibiotic.					DT	28-FEB-2003 (Rel. 41, last sequence update)
FT	DISULFID	7 36 BY SIMILARITY.				DT	28-FEB-2003 (Rel. 41, last annotation update)
FT	DISULFID	14 29 BY SIMILARITY.				DE	50S ribosomal protein L34.
FT	DISULFID	19 37 BY SIMILARITY.				GN	RPMH OR BMEI0276 OR BRA1021.
FT	DISULFID	40 AA; 4649 MW; 9DB6B4E125CEBE30 CRC64;				OS	Brucella melitensis, and
SQ						OS	Brucella suis.
Query Match	100.0%;	Score 15;	DB 1;	Length 40;		OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Best Local Similarity	100.0%;	Score 15;	DB 1;	Length 40;		OC	Brucellaceae; Brucella;
Matches	3;	Conservative 0;	Mismatches 0;	Indels 0;		OX	NCBI_TaxID=29459; 29461;
QY	1	RTR 3				RN	[1]
DB	22 RTR 24					RP	SEQUENCE FROM N.A.
RESULT 12						RC	SPECIES=B_melitensis; STRAIN=16M / ATCC 23456 / Biotype 1;
BD06_BOVIN		STANDARD;	PRT;	42 AA.		RX	MEDLINE-20020109; PubMed-1175668;
ID	BD06_BOVIN		PRT;	42 AA.		RA	Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Benian M.J.,
AC	P46164;					RA	DeVecchio V.G., Kapoor V.J., Patra G., Mujer C., Ios T.,
DT	01-NOV-1995 (Rel. 32, Created)					RA	Ivanova N., Anderson T., Bhattacharyya A., Lykidas A., Reznik G.,
DT	01-FEB-1996 (Rel. 33, Last sequence update)					RA	Jablonski L., Larsen N., D'Souza M., Bernal A., Mazir M., Goltzman E.,
DT	28-FEB-2003 (Rel. 41, last annotation update)					RA	Selkov E., Elzer P.H., Raghuram S., O'Callaghan D., Letesson J.-J.,
DE	Beta-defensin 6 (BNBD-6) (BNBD-6).					RA	Haeleker R., Kyriakis N., Overeem R.;
DE	Beta-defensin 6 (BNBD-6) (BNBD-6).					RA	Brucella melitensis";
GN						RA	Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
OS	Bos taurus (Bovine)					RA	Seitzes N.A.
OC	Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi;					RA	SPECIES=B suis; STRAIN=1330 / Biovar 1;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					RA	MEDLINE-2247741; PubMed-1271122;
OC	Bovidae; Bovinae; Bos.					RA	Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA						RA	Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Benian M.J.,
RA						RA	DeVecchio V.G., Kapoor V.J., Patra G., Mujer C., Ios T.,
RA						RA	Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA						RA	Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA						RA	Kleidermuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA						RA	Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.ish-sib.ch/announce/>
or send an email to license@ish-sib.ch).

CC

DR EMBL; AE001673; AAC19073; 1; -;

DR EMBL; AE002251; AAC38710; 1; -;

DR EMBL; AP002546; BAM99143; 1; -;

DR PIR; A72017; A72017;

DR PIR; B86607; B86607;

DR TIGR; CP0926; -;

DR HAMAP; MF_00391; -; 1.

DR InterPro; IPR000271; Ribosomal_L34.

DR Pfam; PF00468; Ribosomal_L14; 1.

DR ProDom; PDD03101; Ribosomal_L34; 1.

DR TIGRFans; TIGR0103; RIBO Bact; 1.

DR PROSITE; PS0074; RIBOSOMAL_L34; 1.

KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 45 AA; 5548 MW; 1F91D87C8343EE0D CRC64;

Query Match 100.0%; Score 15; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RTR	3
Db	19	RTR	21

Search completed: September 9, 2003, 23:32:15

Job time : 11.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 9, 2003, 23:28:08 ; Search time 45 Seconds

title: US-09-967-003-2

perfect score: 15

Sequence: 1 RTR 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 25802604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL_23;*

1: SP_archaea;*

2: SP_bacteria;*

3: SP_organelle;*

4: SP_human;*

5: SP_invertebrate;*

6: SP_mammal;*

7: SP_mic;*

8: SP_fungi;*

10: SP_plant;*

11: SP_rodent;*

12: SP_virus;*

13: SP_vertebrate;*

14: SP_unclassified;*

15: SP_rvirus;*

16: SP_bacteriap;*

17: SP_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	8 8	019961
2	15	100.0	8 8	019958
3	15	100.0	8 8	019960
4	15	100.0	8 8	019959
5	15	100.0	8 8	019956
6	15	100.0	9 9	019953
7	15	100.0	10 15	087617
8	15	100.0	11 11	08MEP2
9	15	100.0	11 11	08MEP1
10	15	100.0	11 11	08MESS
11	15	100.0	11 11	08MER0
12	15	100.0	11 11	08MER8
13	15	100.0	11 11	08MRS1
14	15	100.0	11 11	08MEP3
15	15	100.0	11 11	08MEQ7
16	15	100.0	11 11	08MEM9
17	15	100.0	11 11	08MER0
18	15	100.0	11 11	08MEM3
19	15	100.0	11 11	08MER5
20	15	100.0	11 11	08MER1
21	15	100.0	11 11	08MER7
22	15	100.0	12 8	08MEP4
23	15	100.0	12 8	08MEQ6
24	15	100.0	12 8	08MEM5
25	15	100.0	12 8	08MEM4
26	15	100.0	12 8	08MER4
27	15	100.0	12 8	08MEQ1
28	15	100.0	12 8	08MEM5
29	15	100.0	12 8	08MEM1
30	15	100.0	12 8	08MEQ8
31	15	100.0	12 8	08MEM2
32	15	100.0	12 8	08MEP7
33	15	100.0	12 8	08MEM5
34	15	100.0	12 8	08MER9
35	15	100.0	12 8	08MEM6
36	15	100.0	12 8	08MEP1
37	15	100.0	12 8	08MEQ4
38	15	100.0	12 8	08MEQ0
39	15	100.0	12 8	08MEM0
40	15	100.0	12 8	08MEP2
41	15	100.0	12 8	08MEQ2
42	15	100.0	12 8	08MER3
43	15	100.0	12 8	08ME6
44	15	100.0	12 8	08MER2
45	15	100.0	12 8	08MEM7

{Without alignments) 17.204 Million cell updates/sec

RESULT 1

ID	PRELIMINARY;	PRT;	8 AA.
019961	019961;	019961;	019961;
AC	AC;	AC;	AC;
DT	DT;	DT;	DT;
DT	01-JAN-1998 (TREMBL_05, Last sequence update)	01-JAN-1998 (TREMBL_05, Last sequence update)	01-JAN-1998 (TREMBL_05, Last sequence update)
DT	01-DEC-2001 (TREMBL_19, Last annotation update)	01-DEC-2001 (TREMBL_19, Last annotation update)	01-DEC-2001 (TREMBL_19, Last annotation update)
DE	DE;	DE;	DE;
DR	Ribosomal protein L16 (Fragment).	Ribosomal protein L16 (Fragment).	Ribosomal protein L16 (Fragment).
GN	GN;	GN;	GN;
OS	Chloroplast.	Chloroplast.	Chloroplast.
OC	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; euRosids II; Malvales; Malvaceae; Malvoideae; Gossypium.	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; euRosids II; Malvales; Malvaceae; Malvoideae; Gossypium.	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; euRosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
NCBI_TaxID	NCBI_TaxID=34276;	NCBI_TaxID=34276;	NCBI_TaxID=34276;
[1]	[1]	[1]	[1]

SEQUENCE FROM N.A.

Small R.L., Ryburn J.A., Cron R.C., Seelanan T., Wendel J.F.; "the tortoise and the hare: choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group"; Am. J. Bot. 85:1501-1515 (1998).

DR EMBL: AFR31456; RAC633550.1; -.

RA Chloroplast.

RT NON_TER FT NON_TER 1

RT SEQUENCE 8 AA: 958 MW: 71B5B73411B40327 CRC64;

RT 8 AA: 958 MW: 71B5B73411B40327 CRC64;

Query Match Similarity 100.0%; Score 15; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTR 3

Db 3 RTR 5

RESULT 2

019958

ID	019958	PRELIMINARY;	PRT;	8 AA.
AC	019958;			
DT	01-JAN-1998 (TREMBLel. 05, Last sequence update)			
DT	01-DEC-2001 (TREMBLel. 19, Last annotation update)			
DE	Ribosomal protein L16 (Fragment).			
RPL16.				
GN				
OS	Gossypium barbadense (Sea-island cotton)	(Egyptian cotton).		
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.			
OX	NCBI_TAXID=3634;			
RN	[1]	SEQUENCE FROM N.A.		
RP				
RA	Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;			
RT	*The tortoise and the hare: choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group.			
RT	Am. J. Bot. 85:1301-1315(1998).			
DR	EMBL; AF031453; AAC63547.1; -.			
RN				
KW	Chloroplast.			
FT	NON_TER 1	1		
FT	NON_TER 8	8		
SQ	SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;			
Query Match	100.0%	Score 15; DB 8; Length 8;		
Best Local Similarity	100.0%	Pred. No. 8.3e+05;		
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 RTR 3			
Db	3 RTR 5			
RESULT 3				
019960				
ID	019960	PRELIMINARY;	PRT;	8 AA.
AC	019960;			
DT	01-JAN-1998 (TREMBLel. 05, Last sequence update)			
DT	01-JAN-1998 (TREMBLel. 05, Last sequence update)			
DE	Ribosomal protein L16 (Fragment).			
RPL16.				
OS	Gossypium mustelinum.			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.			
OX	NCBI_TAXID=34275;			
RN	[1]	SEQUENCE FROM N.A.		
RA	Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;			
RT	*The tortoise and the hare: choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group.;			
RT	Am. J. Bot. 85:1301-1315(1998).			
DR	EMBL; AF031453; AAC63549.1; -.			
RN				
KW	Chloroplast.			
FT	NON_TER 1	1		
FT	NON_TER 8	8		
SQ	SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;			
Query Match	100.0%	Score 15; DB 8; Length 8;		
Best Local Similarity	100.0%	Pred. No. 8.3e+05;		
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 RTR 3			
Db	3 RTR 5			
RESULT 5				
019956				
ID	019956	PRELIMINARY;	PRT;	8 AA.
AC	019956;			
DT	01-JAN-1998 (TREMBLel. 05, Created)			
DT	01-MAR-2002 (TREMBLel. 20, Last sequence update)			
DE	Ribosomal protein L16 (Fragment).			
RPL16.				
OS	Gossypium arboreum (Tree cotton).			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids III; Malvales; Malvaceae; Malvoideae; Gossypium.			
OX	NCBI_TAXID=29729;			
RN	[1]	SEQUENCE FROM N.A.		
RA	Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;			
RT	*The tortoise and the hare: choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group.;			
RT	Am. J. Bot. 85:1301-1315(1998).			
DR	EMBL; AF031451; AAC63545.1; -.			
RN				
KW	Chloroplast.			
FT	NON_TER 1	1		
FT	NON_TER 8	8		
SQ	SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;			
Query Match	100.0%	Score 15; DB 8; Length 8;		
Best Local Similarity	100.0%	Pred. No. 8.3e+05;		
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 RTR 3			
Db	3 RTR 5			

RESULT 4

RESULT 6		08MEM3	PRELIMINARY;	PRT;	9 AA.
ID	08MEM43				
AC	08MEM43;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)				
DE	Ribosomal Protein 16 (Fragment).				
DR	RPL16.				
OS	Howittia trilocularis.				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermato phyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	euroids II; Malvales; Malvaceae; Malvoideae; Sida.				
OX	NCBI_TaxID=183272;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Freil, B.E., Brubaker, C.L., Craven, L.A., Crisp, M.D.;				
RT	*Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using chloroplast DNA sequences of ndhf and the rpl16 intron.;				
RL	Syst. Bot. 27:333-350(2002).				
DR	EMBL: AR384615; AACM50387.1; -.				
KW	Chloroplast.				
FT	NON_TER 1				
FT	NON_TER 1				
SQ	SEQUENCE 9 AA; 1256 MW; 6351D32409D411B4 CRC64;				
Query Match	100.0%; Score 15; DB 8; Length 9;				
Best Local Similarity	100.0%; Pred. No. 8 3e+05;				
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1 RTR 3				
	1 1 1				
Db	2 RTR 4				
RESULT 7		08617	PRELIMINARY;	PRT;	10 AA.
ID	08617				
AC	08617;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Tat protein (Fragment).				
TAT	TAT.				
OS	Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).				
OC	Viruses; Retroviruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=1172;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAINING02;				
RX	MEDLINE=97138325; PubMed=8985351;				
RA	Babillot-Ruché, F., Brengues, C., Galat-Luong, A., Galat, G., Pourrut, X.,				
RA	Vidal, N., Véas, F., Durand, J.P., Cuny, G.;				
RT	*Genetic diversity of simian immunodeficiency viruses from West African green monkeys: evidence of multiple genotypes within populations from the same geographical locale.;				
RT	J. Virol. 71:3071-313(1997).				
DR	EMBL: U37215; AACM56173.1; -.				
NON_TER	1 1				
SQ	SEQUENCE 10 AA; 1148 MW; 83260822D1B411 CRC64;				
Query Match	100.0%; Score 15; DB 15; Length 10;				
Best Local Similarity	100.0%; Pred. No. 5.6e+02;				
Matches	3; Conservative 0; Mismatches 5e+02; Indels 0; Gaps 0;				
Oy	1 RTR 3				
	1 1 1				
Db	4 RTR 6				
RESULT 8		08MEM5	PRELIMINARY;	PRT;	11 AA.
ID	08MEM5				
RP	SEQUENCE FROM N.A.				
RA	Freil, B.E., Brubaker, C.L., Craven, L.A., Crisp, M.D.;				
RT	*Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using chloroplast DNA sequences of ndhf and the rpl16 intron.;				
RL	Syst. Bot. 27:333-350(2002).				
DR	EMBL: AR384616; AACM50388.1; -.				
KW	Chloroplast.				
FT	NON_TER 1				
FT	NON_TER 1				
SQ	SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;				
Query Match	100.0%; Score 15; DB 8; Length 11;				
Best Local Similarity	100.0%; Pred. No. 6.1e+02;				
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1 RTR 3				
	1 1 1				
Db	2 RTR 4				
RESULT 9		08MEM2	PRELIMINARY;	PRT;	11 AA.
ID	08MEM2				
AC	08MEM2;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)				
DE	Ribosomal protein 16 (Fragment).				
DR	RPL16.				
OS	Lagunaria patersonia.				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermato phyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	euroids II; Malvales; Malvaceae; Malvoideae; Lagunaria.				
OX	NCBI_TaxID=183274;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Freil, B.E., Brubaker, C.L., Craven, L.A., Crisp, M.D.;				
RT	*Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using chloroplast DNA sequences of ndhf and the rpl16 intron.;				
RL	Syst. Bot. 27:333-350(2002).				
DR	EMBL: AR384616; AACM50388.1; -.				
KW	Chloroplast.				
FT	NON_TER 1				
FT	NON_TER 1				
SQ	SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;				
Query Match	100.0%; Score 15; DB 8; Length 11;				
Best Local Similarity	100.0%; Pred. No. 6.1e+02;				
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1 RTR 3				
	1 1 1				
Db	2 RTR 4				
RESULT 10		08MEM5	PRELIMINARY;	PRT;	11 AA.

AC 08MESS5; DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Abelmoschus manihot.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 eurosid II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
 OC NCBI_TaxID=183220;
 RN [1] SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RP RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of nadHF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384569; AAC50407.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;
 Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTR 3
 1 11
 Db 2 RTR 4

RESULT 11
 08MEO0 PRELIMINARY; PRT; 11 AA.
 ID 08MEO0 AC
 AC 08MEO0; DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus peralbus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 eurosid II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OC NCBI_TaxID=183256;
 RN [1] SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of nadHF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384598; AAC50370.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;
 Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 1 11
 Db 2 RTR 4

RESULT 13
 08MES1 PRELIMINARY; PRT; 11 AA.
 ID 08MES1 AC
 AC 08MES1; DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Alyogyne pinoniana.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 eurosid II; Malvales; Malvaceae; Malvoideae; Alyogyne.
 OC NCBI_TaxID=183226;
 RN [1] SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of nadHF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL: AF384566; AAC50404.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;
 Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTR 3
 1 11
 Db 2 RTR 4

RESULT 14
 08MFP3 PRELIMINARY; PRT; 11 AA.
 ID 08MFP3 AC
 AC 08MFP3; DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBrel, 22, Last sequence update)
 DT 01-OCT-2002 (TREMBrel, 22, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermato phyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Malvales; Malvaceae; Malvoideae; Hibiscus.
 NCBI_TAXID=183253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil, B. E., Brubaker, C. L., Craven, L. A., Crisp, M. D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 EMBL: AF84555; AAM50353.1;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1470 MW: 72270351D32409D4 CRC64;
 Query Match 100.0%; Score 15; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Ov 1 RTR 3
 DB 2 RTR 4

RESULT 15

OBMEO7	ID	OBMEO7	PRELIMINARY;	PRT;	11 AA.
AC 08MEO7;	DT 01-OCT-2002 (TREMBrel, 22, Created)	DT 01-OCT-2002 (TREMBrel, 22, Last sequence update)	DE Ribosomal protein 16 (Fragment).	GN RPL16.	OS Hibiscus drummondii.
OC Chloroplast.	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	OC Malvales; Malvaceae; Malvoideae; Hibiscus.	NCBI_TAXID=183253;	NCBI_TAXID=183253;
RN [1] SEQUENCE FROM N.A.	RA Pfeil, B. E., Brubaker, C. L., Craven, L. A., Crisp, M. D.;	RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using chloroplast DNA sequences of ndhF and the rpl16 intron.";	RL Syst. Bot. 27:333-350(2002). EMBL: AF84555; AAM50353.1;	KW Chloroplast.	FT NON_TER 1 1 FT NON_TER 11 11 SQ SEQUENCE 11 AA: 1470 MW: 72270351D32409D4 CRC64;
Query Match 100.0%; Score 15; DB 8; Length 11; Best Local Similarity 100.0%; Pred. No. 6.1e+02; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 RTR 3	1 RTR 4	2 RTR 4	3 RTR 4	4 RTR 4

Search completed: September 9, 2003, 23:34:24
 Job time : 48 secs

genCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 9, 2003, 23:20:43 ; Search time 75 seconds

[without alignments] 10.582 Million cell updates/sec.

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTRGG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19jun03:*

1: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA2003.DAT:*

RESULT	1
ID	AAB21218 standard; peptide; 5 AA.
XX	
AC	AAB21218;
XX	
DT	23-FEB-2001 (first entry)
XX	
DE	Synthetic complementary peptide.
XX	
KW	Polymorphonuclear leukocyte; PMN: ophthalmological; antiinflammatory; neutrophil inhibitor; eye disease; alkali-injured eye; chemically injured eye; inflammatory eye disease.
XX	
OS	Synthetic.
XX	
PH	Key
FT	Modified-site
FT	5 /note= "C-terminal amide"
PN	W020053621-A2.
XX	
PD	14-SEP-2000.
XX	
PF	08-MAR-2000; 2000WO-US06062.
XX	
PR	09-MAR-1999; 99US-0123409.
XX	
PA	(HADDY) HADDOCK J L.
PA	(BLA) BLATOCK J E.
PA	(PFTS/) PFISTER R R.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	21	AAB21218
2	27	100.0	7	21	AAB21218
3	27	100.0	8	21	AAB21219
4	27	100.0	8	21	AAB21222
5	27	100.0	10	22	AAG87239
6	27	100.0	10	22	AAG7602
7	27	100.0	32	22	AAG8229
8	27	100.0	41	22	AAG8229
9	27	100.0	50	22	AAU59446

Propionibacterium
Human ORRX Protein
Phascolin Promoter
Phascolin Promoter
Soybean alpha-D- β -D-glucosidase
Human secretory protein
Propionibacterium
Propionibacterium
Human ORRX Protein
Propionibacterium
Human novel protein
Propionibacterium
Propionibacterium
Human immune/Hemagglutinin
N. gonorrhoeae ami
Human ORRX ORP272
Human ORRX protein
Human protein sequ
Oleosin/hirudin protein
Human polypeptide
Zea mays protein f
Novel human diagno
C glutamicum prote
A. thaliana oleosin
Arabidopsis thaliana
Arabidopsis thaliana
A. thaliana oleosin
Arabidopsis thaliana
Propionibacterium
Pan troglodytes oil
Arabidopsis thaliana
Phaseolus vulgaris
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
A. thaliana oleosin
Arabidopsis thaliana
Propionibacterium

XX	DR	09-MAR-1999;	99US-0123409.
XX	PR		
PT	XX	Pharmaceutical composition for treating eye diseases, comprises a peptide having sequence complementary to a specified sequence -	
XX	XX		
PA	XX	Claim 3; Fig 1; 42pp; English.	
PA	XX		
PA	XX	The Present sequence is a synthetic complementary tetrameric peptide which is an antagonist of the polymorphonuclear leukocyte (PMN) chemoattractant, N-acetyl-PGP. It is useful for inhibiting PMN polarisation, chemotaxis and infiltration into tissue activated by neutrophil chemoattractant such as N-acetyl-PGP, N-acetyl-PGX, N-methyl-PGP, or small peptide chemoattractants containing proline and glycine. It may be used for treating eye diseases for e.g. alkali-injured eye, chemically injured eye and inflammatory eye disease.	
PA	XX		
PA	XX	XX Sequence 8 AA;	
PA	XX	Query Match 100.0%; Score 27; DB 21; Length 8; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 RTRGG 5 Db 1 RTRGG 5	
PA	XX		
PA	XX	XX Result 4	
PA	XX	Query Match 100.0%; Score 27; DB 21; Length 8; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 RTRGG 5 Db 1 RTRGG 5	
PA	XX		
PA	XX	XX AAB2122 standard; peptide; 8 AA.	
PA	XX		
PA	XX	XX AAB2122; 23-FEB-2001 (first entry)	
PA	XX		
PA	XX	XX RTR tetramer containing dextrorotatory RTR sequences.	
PA	XX		
PA	XX	XX Polymorphonuclear leukocyte; PMN; ophthalmological; antiinflammatory; chemoattractant; antagonist; N-acetyl-PGP; N-acetyl-PGX; N-methyl-PGP; chemically injured eye; inflammatory eye disease; RTR tetramer.	
PA	XX		
PA	XX	XX Synthentic.	
PA	XX		
PA	XX	XX Key	
PA	XX	XX Peptide	
PA	XX	XX 1.5	
PA	XX	XX /note- "synthetic complementary peptide RTRGG"	
PA	XX	XX Misc-difference 1	
PA	XX	XX /note- "D-form residue"	
PA	XX	XX Misc-difference 2	
PA	XX	XX /note- "D-form residue"	
PA	XX	XX Misc-difference 3	
PA	XX	XX /note- "D-form residue"	
PA	XX	XX Modified-site 6	
PA	XX	XX /note- "Lys(6) is linked to one copy of the RTRGG peptide through the alpha amino group; and to a second copy of the peptide (not shown) via the omega amino group"	
PA	XX	XX Modified-site 7	
PA	XX	XX /note- "the alpha amino group of Lys (7) forms a peptide linkage with the carboxyl group of Lys(6); the omega amino group of Lys(7) forms a peptide bond with a second Lys residue analogous to Lys(6)"	
PA	XX	XX Modified-site 8	
PA	XX	XX /note- "C-terminal amide"	
PA	XX	XX WO20053621-A2.	
PA	XX		
PA	XX	XX 14-SEP-2000.	
PA	XX		
PA	XX	XX 08-MAR-2000; 2000WO-US06062.	
PA	XX		
PA	XX	XX (HADD/) HADDOX J L.	
PA	XX	XX (BLAL/) BLALOCK J E.	
PA	XX	XX (PFIS/) PFISTER R R.	
PA	XX	XX (VILL/) VILLAIN M.	
PA	XX		
PA	XX	XX Haddox JL, Blalock JE, Pfister RR, Villain M;	
PA	XX		
PA	XX	XX DR WPI; 2000-611433/58.	
PA	XX		
PA	XX	XX PT Pharmaceutical composition for treating eye diseases, comprises a peptide having sequence complementary to a specified sequence -	
PA	XX		
PA	XX	XX PS Claim 3; Fig 1; 42pp; English.	
PA	XX		
PA	XX	XX The Present sequence is a synthetic complementary tetrameric peptide which is an antagonist of the polymorphonuclear leukocyte (PMN) chemoattractant, N-acetyl-PGP. It is useful for inhibiting PMN polarisation, chemotaxis and infiltration into tissue activated by neutrophil chemoattractant such as N-acetyl-PGP, N-acetyl-PGX, N-methyl-PGP, or small peptide chemoattractants containing proline and glycine. It may be used for treating eye diseases for e.g. alkali-injured eye, chemically injured eye and inflammatory eye disease.	
PA	XX		
PA	XX	XX Sequence 8 AA;	
PA	XX	Query Match 100.0%; Score 27; DB 21; Length 8; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 RTRGG 5 Db 1 RTRGG 5	
PA	XX		
PA	XX	XX Result 5	
PA	XX	Query Match 100.0%; Score 27; DB 21; Length 8; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 RTRGG 5 Db 1 RTRGG 5	
PA	XX		
PA	XX	XX AAG87237	
PA	XX	XX ID AAG87237 standard; Peptide; 10 AA.	
PA	XX		
PA	XX	XX AC AAC87237;	
PA	XX		
PA	XX	XX DT 11-SEP-2001 (first entry)	
PA	XX		
PA	XX	XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2186.	
PA	XX		
PA	XX	XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification; drug discovery; drug design.	
PA	XX		
PA	XX	XX OS Saccharomyces cerevisiae.	
PA	XX		
PA	XX	XX PN WO200142276-A1.	
PA	XX		
PA	XX	XX PD 14-JUN-2001.	
PA	XX		
PA	XX	XX PF 13-DEC-2000; 2000WO-GB04773.	
PA	XX		
PA	XX	XX PR 13-DEC-1999; 99GB-0029471.	
PA	XX		
PA	XX	XX PA (PROT-) PROTEOM LTD.	
PA	XX		
PA	XX	XX PI Roberts GW, Heal JR;	
PA	XX		
PA	XX	XX DR WPI; 2001-367863/38.	
PA	XX		
PA	XX	XX PT Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design -	
PA	XX		
PA	XX	XX Example 3; Page 331, 488pp; English.	
PA	XX		
PA	XX	XX CC The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher	

CC eukaryotic genomes, excluding human and plants. The specific CC complementary peptides interact with their relevant target proteins CC encoded in the eukaryote genome. The peptides may be used as reagents CC and drugs for drug discovery and as lead ligands for drug design and CC development. The present sequence is a complementary peptide from CC *Saccharomyces cerevisiae*.
XX

Query Match 100.0%; Score 27; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0
 QY 1 RFRGG 5
 1111
 Db 4 RFRGG 8

RESULT 6
AAG87239
ID: AAG87239 standard: pentide: 10 aa
PD
XX
PP
28-SEP-2000; 2000W0-US26524
XX
PP
00 000 1000 0000 015123

XX
AC
XX
XX
DT
XX
DE
XX
XX
AXG87239;
11-SEP-2001 (first entry)
Saccharomyces cerevisiae peptide, SEQ ID NO: 2188.

XX
PR 13-DEC-1999; 99GB-0029471.
XX PA (PROT-) PROTEOM LTD.
XX PT Roberts CW Heal IP.

XX
XX
DR
XX
WPI; 2001-367863/38.
PT
Identifying complementary peptides by analysis of protein and
nucleotide sequence databases, useful in drug design -

PS Example 3; Page 331; 488pp; English.
XX
CC The invention relates to the identification sequence of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC

complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from *Saccharomyces cerevisiae*.

Query Match 100 0%; Score 27; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 7
AAMB2229;
AC
XX
07-NOV-2001 (first entry)

XX	Human immune/haematopoietic antigen	SEQ ID NO:9822.	PR	14-SEP-2000;	2000US-0233065.
DE			PR	21-SEP-2000;	2000US-0234223.
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		PR	21-SEP-2000;	2000US-0234274.
KW	cytostatic; gene therapy; vaccine; metastasis.		PR	25-SEP-2000;	2000US-0234997.
KW			PR	25-SEP-2000;	2000US-0234998.
OS	Homo sapiens.		PR	26-SEP-2000;	2000US-0235484.
XX			PR	27-SEP-2000;	2000US-0235834.
PN	W0200157182-A2.		PR	27-SEP-2000;	2000US-0235836.
XX			PR	29-SEP-2000;	2000US-0236327.
PD	09-AUG-2001.		PR	29-SEP-2000;	2000US-0236367.
XX			PR	29-SEP-2000;	2000US-023568.
PF	17-JAN-2001; 2001WO-US01354.		PR	29-SEP-2000;	2000US-0236369.
PR	31-JAN-2000; 2000US-0179065.		PR	29-SEP-2000;	2000US-0236370.
PR	04-FEB-2000; 2000US-0180628.		PR	02-OCT-2000;	2000US-0236802.
PR	24-FEB-2000; 2000US-0184664.		PR	02-OCT-2000;	2000US-0237037.
PR	02-MAR-2000; 2000US-0186350.		PR	03-OCT-2000;	2000US-0237038.
PR	16-MAR-2000; 2000US-0189874.		PR	03-OCT-2000;	2000US-0237039.
PR	17-MAR-2000; 2000US-0190076.		PR	13-OCT-2000;	2000US-0239935.
PR	18-APR-2000; 2000US-0198123.		PR	13-OCT-2000;	2000US-0239937.
PR	19-MAY-2000; 2000US-0205515.		PR	20-OCT-2000;	2000US-0240960.
PR	07-JUN-2000; 2000US-0209467.		PR	20-OCT-2000;	2000US-0241221.
PR	28-JUN-2000; 2000US-0214886.		PR	20-OCT-2000;	2000US-0241785.
PR	30-JUN-2000; 2000US-0215135.		PR	20-OCT-2000;	2000US-0237039.
PR	07-JUL-2000; 2000US-0216647.		PR	20-OCT-2000;	2000US-0241787.
PR	07-JUL-2000; 2000US-0216880.		PR	20-OCT-2000;	2000US-0241808.
PR	11-JUL-2000; 2000US-0217487.		PR	20-OCT-2000;	2000US-0241809.
PR	11-JUL-2000; 2000US-0217496.		PR	20-OCT-2000;	2000US-0241826.
PR	14-JUL-2000; 2000US-0218290.		PR	01-NOV-2000;	2000US-0244617.
PR	26-JUL-2000; 2000US-0220963.		PR	08-NOV-2000;	2000US-0244786.
PR	14-AUG-2000; 2000US-0220964.		PR	08-NOV-2000;	2000US-0244775.
PR	14-AUG-2000; 2000US-0224518.		PR	08-NOV-2000;	2000US-0244647.
PR	07-JUL-2000; 2000US-0216880.		PR	08-NOV-2000;	2000US-0244647.
PR	14-AUG-2000; 2000US-0224519.		PR	08-NOV-2000;	2000US-0244647.
PR	11-JUL-2000; 2000US-0217496.		PR	08-NOV-2000;	2000US-0244647.
PR	14-AUG-2000; 2000US-0225314.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225358.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225366.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225367.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225370.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225371.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225375.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225378.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225379.		PR	08-NOV-2000;	2000US-0244652.
PR	14-AUG-2000; 2000US-0225379.		PR	08-NOV-2000;	2000US-0244652.
PR	18-AUG-2000; 2000US-0226279.		PR	08-NOV-2000;	2000US-0244652.
PR	22-AUG-2000; 2000US-0226681.		PR	08-NOV-2000;	2000US-0244652.
PR	22-AUG-2000; 2000US-0226868.		PR	08-NOV-2000;	2000US-0244652.
PR	22-AUG-2000; 2000US-0227182.		PR	08-NOV-2000;	2000US-0244652.
PR	23-AUG-2000; 2000US-0227009.		PR	08-NOV-2000;	2000US-0244652.
PR	30-AUG-2000; 2000US-0228924.		PR	08-NOV-2000;	2000US-0244652.
PR	01-SEP-2000; 2000US-0229387.		PR	08-NOV-2000;	2000US-0244652.
PR	01-SEP-2000; 2000US-0229433.		PR	08-NOV-2000;	2000US-0244652.
PR	01-SEP-2000; 2000US-0229434.		PR	17-NOV-2000;	2000US-0244652.
PR	01-SEP-2000; 2000US-0229444.		PR	17-NOV-2000;	2000US-0244652.
PR	01-SEP-2000; 2000US-0229444.		PR	17-NOV-2000;	2000US-0244652.
PR	05-SEP-2000; 2000US-0225059.		PR	17-NOV-2000;	2000US-0244652.
PR	05-SEP-2000; 2000US-0229513.		PR	17-NOV-2000;	2000US-0244652.
PR	06-SEP-2000; 2000US-0230337.		PR	17-NOV-2000;	2000US-0244652.
PR	06-SEP-2000; 2000US-0230438.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0231242.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0231243.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0231244.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0231413.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0231414.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0232080.		PR	17-NOV-2000;	2000US-0244652.
PR	08-SEP-2000; 2000US-0232081.		PR	17-NOV-2000;	2000US-0244652.
PR	12-SEP-2000; 2000US-0231968.		PR	17-NOV-2000;	2000US-0244652.
PR	14-SEP-2000; 2000US-0232397.		PR	17-NOV-2000;	2000US-0244652.
PR	14-SEP-2000; 2000US-0232398.		PR	17-NOV-2000;	2000US-0244652.
PR	14-SEP-2000; 2000US-0232399.		PR	17-NOV-2000;	2000US-0244652.
PR	14-SEP-2000; 2000US-0232400.		PR	17-NOV-2000;	2000US-0244652.
PR	14-SEP-2000; 2000US-0232401.		PR	17-NOV-2000;	2000US-0244652.
PR	14-SEP-2000; 2000US-02323063.		PR	01-DEC-2000;	2000US-0251866.
PR	14-SEP-2000; 2000US-0233064.		PR	08-DEC-2000;	2000US-0251869.

XX	PA	(CORI-X) CORIXA CORP.
XX	PR	30-MAY-2000; 2000US-206132P.
XX	PR	29-AUG-2000; 2000US-228716P.
XX	PA	(CURA-) CURAGEN CORP.
XX	PR	WPI; 2001-616774/71.
XX	DR	N-PSB; AAS59657.
XX	PR	Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
XX	PS	Example 1; SEQ ID No 28946; 1069pp; English.
XX	CC	Sequences AAB39105-AAB68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by <i>P. acnes</i> . The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis. <i>P. acnes</i> is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of <i>P. acnes</i> in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for <i>P. acnes</i> proteins. These antibodies can be used to downregulate expression and activity of <i>P. acnes</i> polypeptides and therefore treat <i>P. acnes</i> infections. The antibodies may also be used as diagnostic agents for determining <i>P. acnes</i> presence, for example, by enzyme linked immunosorbent assay (ELISA).
XX	CC	Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences .
XX	SQ	Sequence 50 AA;
XX	Query Match	100 %; Score 27; DB 22; Length 50;
XX	Best Local Similarity	100.0%; Pred. No. 1.7e+02;
XX	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	RTRGG 5
AC	1111	
DB	29	RTRGG 33
XX	RESULT 11	
XX	ABP00475	
XX	ID	ABP00475 standard; Protein; 52 AA.
XX	AC	ABP00475;
XX	DT	24-JUN-2002 (first entry)
XX	DE	Human ORFX protein sequence SEQ ID NO:932.
XX	KW	Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis; Homo sapiens.
XX	OS	W0200102523-A2.
XX	PN	06-DEC-2001.
XX	PD	29-MAY-2001; 2001WO-US10836.
XX	PR	Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
XX	PS	Disclosure; SEQ ID 932; 107pp; English.
XX	CC	The present invention describes substantially purified human proteins (referred to as open reading frame, ORFx, where x is 1-11491 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFx proteins given in ABP0010 to ABP0010. ORFx proteins are useful for treating or preventing a pathology associated with an ORFx-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFx-associated disorder. ORFx polynucleotide sequences can be used in gene therapy. ORFx sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFx proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
XX	CC	N.B. The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences .
XX	SQ	Sequence 52 AA;
XX	Query Match	100.0%; Score 27; DB 23; Length 52;
XX	Best Local Similarity	100.0%; Pred. No. 1.7e+02;
XX	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	RTRGG 5
AC	1111	
DB	5	RTRGG 9
XX	RESULT 12	
XX	ABP00684	
XX	ID	ABP00684 standard; Protein; 55 AA.
XX	AC	ABP00684;
XX	DT	06-SEP-2002 (first entry)
XX	DE	Phaseolin promoter-Trxh oleosin-phaseolin terminator SEQ:21.
XX	KW	Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; cytostatic; antisporic; vasotropin; milk; wheat; oxidative stress; catarract; diabetes; chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis; bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing; gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX	KW	gastro oesophageal reflux disease.

OS	Arabidopsis sp.	KW	chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
OS	Phaseolus vulgaris.	KW	bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
XX		KW	gastro intestinal bleeding; intestinal bowel disease; ulcer;
PN		KW	gastro oesophageal reflux disease.
XX	WO200250289-A1.		
PD	27-JUN-2002.		
XX			
PF	19-DEC-2001; 2001WO-US50240.		
XX			
PR	19-DEC-2000; 2000US-0742900.		
PR	05-JUL-2001; 2001US-302885P.		
PR	04-DEC-2001; 2001US-006038.		
XX			
PA	(SYMB-) SEMBIOSYS GENETICS INC.		
PA	(SYGN-) SYNGENTA PARTICIPATIONS AG.		
XX			
PT	Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;		
PI	Del Val G, Zaplachinski S, Moloney M;		
XX			
PT	WPI; 2002-508806/54.		
DR	N-PSDB; ABN89581.		
XX			
PT	producing oil body associated with recombinant multimeric protein		
PT	complex e.g. redox proteins and immunoglobulins comprises producing		
PT	recombinant polypeptides capable of forming the complex in cells		
PT	comprising oil bodies -		
XX			
PS	Disclosure: Page 172; 362PP; English.		
XX			
CC	The present invention describes a method (M1) for producing an oil body		
CC	associated with a recombinant multimeric protein complex (MPC). M1		
CC	comprises producing in a cell comprising oil bodies a first and second		
CC	recombinant polypeptide (P1, P2), where P1 is capable of associating		
CC	with P2 to form the MPC and associating the complex with an occlusion		
CC	body (OB) through an OB-targeting protein capable of associating with OB		
CC	and P1. M1 is useful for producing an oil body associated with a		
CC	recombinant MPC. The oil bodies are further formulated for use in the		
CC	preparation of a food product such as milk or wheat based food product,		
CC	personal care product which reduces the oxidative stress on the surface		
CC	area of the human body or used to lighten the skin, or a pharmaceutical		
CC	composition used to treat chronic obstructive pulmonary disease (COPD),		
CC	cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis,		
CC	malignancies, reperfusion injury, wound healing, sepsis, gastro		
CC	intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD		
CC	(gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP6077		
CC	to ABP6064 represent sequence given in the exemplification of the		
CC	present invention.		
XX			
SQ	Sequence 55 AA;		
Query Match	100.0%; Score 27; DB 23; Length 55;		
Best Local Similarity	100.0%; Pred. No. 1.8e+02;		
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 RTRGG 5		
Db	47 RTRGG 51		
RESULT 13			
ABP60689			
ID	ABP60689; standard; Protein; 55 AA.		
XX			
AC	ABP60689;		
XX			
DT	06-SEB-2002 (first entry)		
XX			
DE	Phaseolin promoter-thioredoxin reductase oleosin-terminator SEQ:29.		
XX			
KW	Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;		
KW	oil body; ophthalmological; antidiabetic; cytostatic; antisorbative;		
KW	vasotropics; pulmonary; antibacterial; immunosuppressive; antiulcer;		
KW	food product; milk; wheat; oxidative stress; cataract; diabetes;		
DE	Soybean alpha-D-galactosidase signal peptide.		
RESULT 14			
ABW10323			
ID	ABW10323 standard; Peptide; 59 AA.		
XX			
AC	ABW10323;		
XX			
DT	03-MAY-1997 (first entry)		
XX			

XX	KW	Alpha-D-galactosidase; soybean; deantigenation enzyme;	XX	PR	05-SEP-2000; 2000US-229747P.
XX	KW	blood type O; antigen; seroconversion; blood transfusion;	XX	PR	05-SEP-2000; 2000US-229748P.
XX	KW	erythrocyte.	XX	PR	05-SEP-2000; 2000US-229749P.
OS	OS	Glycine max.	XX	PR	05-SEP-2000; 2000US-229750P.
XX	XX	W09640714-A1.	XX	PR	05-SEP-2000; 2000US-229751P.
PN	PN	19-DEC-1996.	XX	PR	05-SEP-2000; 2000US-229516P.
XX	PF	08-MAY-1996; 9640-0506511.	XX	PR	05-SEP-2000; 2000US-229517P.
XX	PR	07-JUN-1995; 950US-048861.	XX	PR	05-SEP-2000; 2000US-230518P.
PR	PR	08-SEP-1994; 940US-0303156.	XX	PR	05-SEP-2000; 2000US-230519P.
XX	PA	(UMOR) UNIV MISSOURI.	XX	PR	05-SEP-2000; 2000US-230519P.
XX	PA	Smith DS, Walker JC;	XX	PR	06-SEP-2000; 2000US-230598P.
XX	XX	WPI: 1997-05215-05.	XX	PR	06-SEP-2000; 2000US-230599P.
DR	DR	N-PSDB; AAT47065.	XX	PR	06-SEP-2000; 2000US-230599P.
XX	PT	Recombinant alpha-D-galactosidase(s) from Glycine and Phaseolus -	XX	PR	06-SEP-2000; 2000US-230599P.
CC	CC	are encoded by a cDNA clone (AAT47065) isolated from a soybean cDNA library. The mature enzyme can be used to convert type B erythrocytes to	XX	PR	06-SEP-2000; 2000US-230599P.
CC	CC	type O cells for blood transfusion	XX	PR	06-SEP-2000; 2000US-230865P.
XX	PS	Example 6; Page 42; 61pp; English.	XX	PR	06-SEP-2000; 2000US-230865P.
XX	Qy	A signal peptide (AAW1033) and mature alpha-D-galactosidase (AAW10320) are encoded by a cDNA clone (AAT47065) isolated from a soybean cDNA library. The mature enzyme can be used to convert type B erythrocytes to type O cells for use in blood transfusions.	XX	PR	06-SEP-2000; 2000US-230988P.
XX	SO	Query Match 100.0%; Score 27; DB 18; Length 59;	XX	PR	06-SEP-2000; 2000US-230988P.
XX	PS	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	XX	PR	06-SEP-2000; 2000US-230990P.
XX	PS	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	PR	06-SEP-2000; 2000US-230897P.
XX	XX	Sequence 59 AA;	XX	PR	07-SEP-2000; 2000US-230951P.
XX	XX	PR	07-SEP-2000; 2000US-231163P.		
XX	XX	PR	07-SEP-2000; 2000US-231832P.		
XX	XX	(INCY-) INCYTE GENOMICS INC.	XX	PR	07-SEP-2000; 2000US-231832P.
PA	PA	Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PI	Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PI	Momilama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PI	Gerstlin EH, Peraita CH, David MH, Panzer SR, Flores V, Daffo A;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PI	Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	DR	WPI; 2002-315658/35.	XX	PR	07-SEP-2000; 2000US-231832P.
XX	N-PSDB	N-PSDB; AAT47065.	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PT	Polynucleotide sequences encoding human secretory proteins useful for	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PT	gene therapy of e.g. genetic deficiency disorders, cancers, and	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PT	diseases caused by intracellular parasites -	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PS	Claim 29; Page 367; 585PP; English.	XX	PR	07-SEP-2000; 2000US-231832P.
XX	CC	The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and protozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's disease), motor neuron disorders, demyelinating diseases (e.g. multiple sclerosis), meningitis, abscesses, priopneuritis, priopneuritis, cerebral palsy, neuroskeletal disorders, peripheral nervous system disorders, dermatoepididiotis, and polyomysitis, myopathy, myasthenia gravis, and mental disorders (e.g. Tourette's syndrome). Amino acid sequences ABB97749 - ABB97933 represent human secretory proteins of the invention.	XX	PR	07-SEP-2000; 2000US-231832P.
XX	SO	Sequence 60 AA;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	XX	Query Match 100.0%; Score 27; DB 23; Length 60;	XX	PR	07-SEP-2000; 2000US-231832P.
PN	PN	Best Local Similarity 100.0%; Pred. No. 2e+02;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	PS	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	PR	07-SEP-2000; 2000US-231832P.
XX	Qy	1 RTRGG 5	XX	PR	07-SEP-2000; 2000US-231832P.
XX	DB	40 RTRGG 44	XX	PR	07-SEP-2000; 2000US-231832P.

Search completed: September 9, 2003, 23:31:42
Job time : 77 secs

COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4846/021A
FILING DATE: April 25, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Grenell, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 9369-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-846-021A-3

Query Match 100.0%; Score 27; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 73; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 47 RTRGG 51

RESULT 3
US-08-488-961-3
; Sequence 3, Application US/08488961
; Patent No. 5606042
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-Galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6184017thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,297
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 0394.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANEDNESS: single
TOPOLGY: linear
US-08-973-297-3

Query Match 100.0%; Score 27; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 78; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 47 RTRGG 46

RESULT 4
US-08-973-297-3
; Sequence 3, Application US/08973297
; Patent No. 6184017
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-Galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6184017thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,297
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 0394.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANEDNESS: single
TOPOLGY: linear
US-08-973-297-3

RESULT 5
PC-05511-3
; Sequence 3, Application PC/TUS9606511
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.
; TITLE OF INVENTION: Glycine and Phaseolus
; TITLE OF INVENTION: alpha-D-Galactosidases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates

STREET: 30500 Northwestern Hwy., Suite 410
 CITY: Farmington Hills
 STATE: Michigan
 COUNTRY: US
 ZIP: 48334

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06511
 FILING DATE:
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30, 955
 REFERENCE/DOCKET NUMBER: 0094, 00050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (810) 539-5050
 TELEFAX: (810) 539-5055
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 59 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PCT-US96-06511-3

RESULT 6
 US-09-252-991A-19703
 Sequence 19703, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Rubenfeld et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107195, 136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60,074, 788
 PRIOR FILING DATE: 1998-02-18
 APPLICATION NUMBER: US 60/094, 190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 19703
 LENGTH: 121
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19703

Query Match 100.0%; Score 27; DB 5; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 42 RTRGG 46

PCT-US96-06511-3

GENERAL INFORMATION:
 APPLICANT: Motonev, Maurice
 APPLICANT: Boothe, Joseph
 APPLICANT: Van Rooijen, G.J.S
 TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/767, 026
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gravelle, Micheline
 REGISTRATION NUMBER: 40,261
 REFERENCE/DOCKET NUMBER: 9369-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 125 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-767-026-5

Query Match 100.0%; Score 27; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 47 RTRGG 51

RESULT 8

US-09-319-275A-5
 Sequence 5, Application US/09319275A
 Patent No. 6509453

GENERAL INFORMATION:

APPLICANT: Moloney, Maurice
 APPLICANT: Boothe, Joseph
 APPLICANT: Roeljen, G.J.S Van
 TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
 FILE REFERENCE: 9369-85
 CURRENT APPLICATION NUMBER: US/09/319, 275A
 CURRENT FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: US 08/767, 026
 PRIOR FILING DATE: 1997-12-16
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 5
 LENGTH: 125

TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Oleosin - Hirudin Fusion

RESULT 7
 US-09-767-026-5
 Sequence 5, Application US/08767026
 Patent No. 5856452
 Query Match 100.0%; Score 27; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;

US-09-319-275A-5
 Query Match 100.0%; Score 27; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 Db 47 RTRGG 51

RESULT 9
 US-09-732-210-1664
 Sequence 1664, Application US/09732210
 Patent No. 5573361

GENERAL INFORMATION:
 APPLICANT: Bunkers, Greg J.
 APPLICANT: Liang, Jihong
 APPLICANT: Mittanck, Cindy A.
 APPLICANT: Seale, Jeffrey W.
 APPLICANT: Wu, Yonne S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 FILE REFERENCE: 38-21115036(B)
 CURRENT APPLICATION NUMBER: US/09732.210
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,513
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: US 60/169,340
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 1753
 SEQ ID NO 1664
 LENGTH: 129
 TYPE: PRT
 ORGANISM: Methanococcus jannaschii
 US-09-732-210-1664

Query Match 100.0%; Score 27; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 Db 48 RTRGG 52

RESULT 10
 US-09-252-991A-21581
 Sequence 21581, Application US/09252991A
 Patent No. 6551795

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSUDOMONAS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 21581
 LENGTH: 142
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-21581

Query Match 100.0%; Score 27; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-09-252-991A-21581

Query Match 100.0%; Score 27; DB 4; Length 142;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Db 11 RTRGG 15

RESULT 12
 US-08-366-783-2
 Sequence 2, Application US/08366783
 Patent No. 5620554

GENERAL INFORMATION:
 APPLICANT: Moloney, Maurice M
 TITLE OF INVENTION: Oil-Body Proteins As Carriers Of
 TITLE OF INVENTION: High-Value Peptides In Plants
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DEHLINGER & ASSOCIATES
 STREET: 350 CAMBRIDGE AVENUE, SUITE 250
 CITY: PALO ALTO
 STATE: California
 COUNTRY: United States
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release 1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,783
 FILING DATE:
 CLASSIFICATION: 800
 REGISTRATION NUMBER: 33,875
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-324-0880
 TELEFAX: 415-324-0960
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 154 amino acids
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-366-783-5

Query Match 100.0%; Score 27; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Db 146 RTRGG 150

TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-A8/831,575

FILING DATE: 09-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: DIGI DIO, FRANK S

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 10203

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

SEQUENCE INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 173 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-A8/831,575-6

Query Match 100.0%; score 27; DB 2; Length 173;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0;

Matches 5; Conservative 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 165 RTRGG 169

Search completed: September 9, 2003, 23:36:08
Job time : 26.625 secs

OM protein - protein search, using sw model											
Run on:	September 9, 2003, 23:34:34 ; Search time 46.875, Seconds			(without alignments)							
Score:	US-09-967-003-3			14.646 Million cell updates/second							
Sequence:	1 RTGG 5										
Scoring table:	BIOSIM62										
Gapext:	Gapext 10.0 , Gapext 0.5										
Searched:	513375 seqs, 137303645 residues										
Total number of hits satisfying chosen parameters:	513375										
Minimum DB seq length:	0										
Maximum DB seq length:	2000000000										
Post-processing:	Minimum Match 0%										
	Maximum Match 100%										
	Listing first 45 summaries										
Database :	Published_Applications_MM: [*]										
1:	/rcgn2_6/ptodata/1/pubpaas/US07_PUCOMB.pep:*										
2:	/rcgn2_6/ptodata/1/pubpaas/PCTC_NEW_PUB.pep:*										
3:	/rcgn2_6/ptodata/1/pubpaas/US06_NEW_PUB.pep:*										
4:	/rcgn2_6/ptodata/1/pubpaas/US06_PUCOMB.pep:*										
5:	/rcgn2_6/ptodata/1/pubpaas/US07_NEW_PUB.pep:*										
6:	/rcgn2_6/ptodata/1/pubpaas/PCTC_NEW_PUCOMB.pep:*										
7:	/rcgn2_6/ptodata/1/pubpaas/US08_NEW_PUB.pep:*										
8:	/rcgn2_6/ptodata/1/pubpaas/PUCOMB.pep:*										
9:	/rcgn2_6/ptodata/1/pubpaas/US09_NEW_PUB.pep:*										
10:	/rcgn2_6/ptodata/1/pubpaas/US09B_PUCOMB.pep:*										
11:	/rcgn2_6/ptodata/1/pubpaas/US09C_PUCOMB.pep:*										
12:	/rcn2_6/ptodata/1/pubpaas/US09_NEW_PUB.pep:*										
13:	/rcn2_6/ptodata/1/pubpaas/US09A_PUCOMB.pep:*										
14:	/rcn2_6/ptodata/1/pubpaas/US09C_PUCOMB.pep:*										
15:	/rcn2_6/ptodata/1/pubpaas/US09C_PUCOMB.pep:*										
16:	/rcn2_6/ptodata/1/pubpaas/US10_NEW_PUB.pep:*										
17:	/rcn2_6/ptodata/1/pubpaas/US10_NEW_PUB.pep:*										
18:	/rcn2_6/ptodata/1/pubpaas/US10_NEW_PUCOMB.pep:*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.											
SUMMARIES											
Result No.	Score	Query Match Length	DB ID	Description							
1	27	100.0	5	US-09-967-003-3	Sequence 3, A						
2	27	100.0	32	US-10-1606-6866	Sequence 6866						
3	27	100.0	44	US-10-037-243-9	Sequence 9, A						
4	27	100.0	55	US-09-897-898-12	Sequence 12, A						
5	27	100.0	55	US-09-897-898-20	Sequence 20, A						
6	27	100.0	55	US-09-893-525-3	Sequence 3, A						
7	27	100.0	125	US-10-260-960-5	Sequence 5, A						
8	27	100.0	125	US-10-260-962-5	Sequence 5, A						
9	27	100.0	146	US-09-738-626-6573	Sequence 6573						
10	27	100.0	162	US-09-741-155-173	Sequence 173,						
11	27	100.0	169	US-09-897-898-9	Sequence 9, A						
12	27	100.0	173	US-10-260-960-2	Sequence 2, A						
13	27	100.0	173	US-10-260-562-5	Sequence 2, A						
14	27	100.0	187	US-09-893-525-5	Sequence 5, A						
15	27	100.0	194	US-09-910-562-4	Sequence 4, A						

Fre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

RESULT 2-698-6866
 Sequence 6866, Application US/10106698
 Publication No. US20030109690A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 CURRENT APPLICATION NUMBER: US/10/106,698
 CURRENT FILING DATE: 2002-03-27
 PRIOR APPLICATION NUMBER: PCT/US00/26524
 PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: US 60/157,137
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: US 60/163,280
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: Patentin Ver. 3.0
 SEQ ID NO 6866
 LENGTH: 32
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: MISC_FEATURE
 LOCATION: (17)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: MISC_FEATURE
 LOCATION: (22)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: MISC_FEATURE
 LOCATION: (23)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: MISC_FEATURE
 LOCATION: (25)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-106-698-6866

Query Match Similarity 100.0%; Score 27; DB 15; Length 32;
 Best Local Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 26 RTRGG 30

RESULT 3
 US-10-037-243-9
 Sequence 9, Application US/10037243
 Publication No. US20030134352A1
 GENERAL INFORMATION:
 APPLICANT: Brookhaven Science Associates, LLC.
 APPLICANT: Freimuth, Paul T
 APPLICANT: Zhang, Yian-Biao
 APPLICANT: Howitt, Jason A
 TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
 FILE REFERENCE: BSA 01-22
 CURRENT APPLICATION NUMBER: US/10/037,243
 CURRENT FILING DATE: 2002-06-03
 NUMBER OF SEQ ID NOS: 46
 SEQ ID NO 9
 LENGTH: 44
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Synthetic T7B3 peptide
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic T7B3 peptide

Query Match Similarity 100.0%; Score 27; DB 12; Length 44;
 Best Local Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-10-037-243-9

RESULT 4-898-12
 Sequence 12, Application US/09897998
 Patent No. US20030137303A1
 GENERAL INFORMATION:
 APPLICANT: DECKERS, HARM M.
 APPLICANT: VAN ROOLIEN, GIJS
 APPLICANT: BOOTHE, JOSEPH
 APPLICANT: GOLL, JANIS
 APPLICANT: DALMIA, BIPIN K.
 TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
 FILE REFERENCE: 034547/0104
 CURRENT APPLICATION NUMBER: US/09/897,898
 CURRENT APPLICATION NUMBER: US/09/897,898
 CURRENT FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: 09/577,147
 PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: 09/448,600
 PRIOR FILING DATE: 1999-11-24
 PRIOR APPLICATION NUMBER: 09/084,777
 PRIOR FILING DATE: 1998-05-27
 PRIOR APPLICATION NUMBER: 60/047,753
 PRIOR FILING DATE: 1997-05-27
 PRIOR APPLICATION NUMBER: 60/047,779
 PRIOR FILING DATE: 1997-05-28
 PRIOR APPLICATION NUMBER: 60/075,863
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/075,864
 PRIOR FILING DATE: 1998-02-25
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 12
 LENGTH: 55
 TYPE: PRT
 ORGANISM: Unknown organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Phaseolin
 OTHER INFORMATION: Description of Unknown Organism: Phaseolin-terminator
 US-09-897-898-12

Query Match Similarity 100.0%; Score 27; DB 9; Length 55;
 Best Local Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 47 RTRGG 51

RESULT 5-898-20
 Sequence 20, Application US/09897998
 Patent No. US20030137303A1
 GENERAL INFORMATION:
 APPLICANT: DECKERS, HARM M.
 APPLICANT: VAN ROOLIEN, GIJS
 APPLICANT: BOOTHE, JOSEPH
 APPLICANT: GOLL, JANIS
 APPLICANT: DALMIA, BIPIN K.
 TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
 FILE REFERENCE: 034547/0104
 CURRENT APPLICATION NUMBER: US/09/897,898
 CURRENT FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: 09/577,147

PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: 09/448,600
 PRIOR FILING DATE: 1999-11-24
 PRIOR APPLICATION NUMBER: 09/084,777
 PRIOR FILING DATE: 1998-05-27
 PRIOR APPLICATION NUMBER: 60/047,753
 PRIOR FILING DATE: 1997-05-27
 PRIOR APPLICATION NUMBER: 60/047,779
 PRIOR FILING DATE: 1997-05-28
 PRIOR APPLICATION NUMBER: 60/075,863
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/075,864
 PRIOR FILING DATE: 1998-02-25
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 20
 LENGTH: 55
 TYPE: PRT
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Phaseolin
 OTHER INFORMATION: promoter-thioredoxin reductase oleosin-phaseolin
 US-09-897-898-20

Query Match 100.0%; Score 27; DB 9; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 1111
 Db 47 RTRGG 51

RESULT 6

US-09-893-525-3

Sequence 3, Application US/09893525

Publication No. US20030126631A1

GENERAL INFORMATION:

APPLICANT: Moloney, Maurice M.

APPLICANT: Van Roijen, G.J.S

TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodies

FILE REFERENCE: 9369-172

CURRENT APPLICATION NUMBER: US/09/893,525

PRIOR APPLICATION NUMBER: US 09/210,843

PRIOR FILING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: US 08/846,021

PRIOR FILING DATE: 1997-04-25

PRIOR APPLICATION NUMBER: US 08/366,783

PRIOR APPLICATION NUMBER: US 08/142,418

PRIOR FILING DATE: 1993-11-16

PRIOR APPLICATION NUMBER: US 07/659,835

PRIOR FILING DATE: 1991-02-22

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.1

SEQ ID NO: 3

LENGTH: 55

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-09-893-525-3

Query Match 100.0%; Score 27; DB 11; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 1111
 Db 47 RTRGG 51

RESULT 8

US-10-260-562-5

Sequence 5, Application US/10260562

Publication No. US20030096320A1

GENERAL INFORMATION:

APPLICANT: Moloney, Maurice M.

APPLICANT: Van Roijen, G.J.S

TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodies

FILE REFERENCE: 9369-172

CURRENT APPLICATION NUMBER: US/09/210,843

PRIOR APPLICATION NUMBER: US 09/319,275

PRIOR FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US 09/319,275

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: US 08/767,026

PRIOR FILING DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

SEQ ID NO: 5

LENGTH: 125

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Oleosin - Hirudin Fusion

US-10-260-562-5

Query Match 100.0%; Score 27; DB 15; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 1111
 Db 47 RTRGG 51

RESULT 9

US-09-738-626-6573

Sequence 6573, Application US/097386573

Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: Moloney, Maurice M.

APPLICANT: Boothe, Joseph

APPLICANT: Roeljen, G.J.S

TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices

FILE REFERENCE: 9369-225

CURRENT APPLICATION NUMBER: US/10/260,960

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US 09/319,275

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: US 08/767,026

PRIOR FILING DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.1

SEQ ID NO: 5

LENGTH: 125

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Oleosin - Hirudin Fusion

US-09-738-626-6573

Query Match 100.0%; Score 27; DB 15; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 1111
 Db 47 RTRGG 51

GENERAL INFORMATION:
 APPLICANT: NAKAGAWA, SATOSHI
 APPLICANT: MIZOGUCHI, HIROSHI
 APPLICANT: ANDO, SPIKO
 APPLICANT: HATASHI, MIKIRO
 APPLICANT: OCHIAI, KEIKO
 APPLICANT: YOKOI, HARUHIKO
 APPLICANT: TATEISHI, NAOKO
 APPLICANT: SENOU, AKIHIRO
 APPLICANT: IKEDA, MASATO
 APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US-09/738, 626
 CURRENT FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: JP 99/377484
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00/159162
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: JP 00/280988
 PRIOR FILING DATE: 2000-08-03
 SOFTWARE: PatentIn ver. 3.0
 SEQ ID NO 6573
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-6573

Query Match 100.0%; Score 27; DB 10; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Dp 53 RTRGG 57

RESULT 10
 US-09-747-155-173
 Sequence 173, Application US/09747155
 Patent No. US200015692A1
 GENERAL INFORMATION:
 APPLICANT: Bouquier, Sylvie
 APPLICANT: Giorgi, Dominique
 TITLE OF INVENTION: No. US20020151692A1 *el Polypeptides and Nucleic Acids Encoding Sam*
 CURRENT APPLICATION NUMBER: US/09/747/, 155
 CURRENT FILING DATE: 2000-12-21
 PRIOR APPLICATION NUMBER: 60/171,746
 PRIOR FILING DATE: 1999-12-22
 NUMBER OF SEQ ID NOS: 431
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 173
 LENGTH: 162
 TYPE: PRT
 ORGANISM: Pan troglodytes
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(487)
 OTHER INFORMATION: Taxon = 9598; gene = PTR205; Accession DDBJ/EMBL/GenBank = AF1797
 US-09-747-155-173

Query Match 100.0%; Score 27; DB 10; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Dp 106 RTRGG 110

RESULT 11
 US-09-897-898-9
 Sequence 9, Application US/09897898
 Patent No. US2002013703A1
 GENERAL INFORMATION:
 APPLICANT: DECKERS, HARM M.
 APPLICANT: VAN ROLLEN, GIJS
 APPLICANT: BOOTHE, JOSEPH
 APPLICANT: GOLL, JANIS
 APPLICANT: MOLONEY, MAURICE M.
 APPLICANT: DALMIA, BIPIN K.
 TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
 FILE REFERENCE: 034547/0104
 CURRENT APPLICATION NUMBER: US/09/897, 898
 CURRENT FILING DATE: 2001-09-21
 PRIOR APPLICATION NUMBER: 09/557, 147
 PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: 09/448, 600
 PRIOR FILING DATE: 1999-11-24
 PRIOR APPLICATION NUMBER: 09/084, 777
 PRIOR FILING DATE: 1998-05-27
 PRIOR APPLICATION NUMBER: 60/047, 753
 PRIOR FILING DATE: 1997-05-27
 PRIOR APPLICATION NUMBER: 60/047, 779
 PRIOR FILING DATE: 1997-05-28
 PRIOR APPLICATION NUMBER: 60/075, 863
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/075, 864
 PRIOR FILING DATE: 1998-02-25
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 169
 TYPE: PRT
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Phaseolin
 OTHER INFORMATION: OTHER INFORMATION: promoter-oleosin Txn-phaseolin terminator
 US-09-897-898-9

Query Match 100.0%; Score 27; DB 9; Length 169;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Dp 47 RTRGG 51

RESULT 12
 US-10-260-960-2
 Sequence 2, Application US/10260960
 Publication No. US20030059910A1
 GENERAL INFORMATION:
 APPLICANT: Moloney, Maurice
 APPLICANT: Boothe, Joseph
 APPLICANT: Roolien, Gijjs Van
 TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
 FILE REFERENCE: 9159-225
 CURRENT APPLICATION NUMBER: US/10/260, 960
 CURRENT FILING DATE: 2002-10-01
 PRIOR APPLICATION NUMBER: US 09/319, 275
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: US 08/767, 026
 PRIOR FILING DATE: 1997-12-16
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 173
 TYPE: PRT
 ORGANISM: Arabidopsis Thaliana
 US-10-260-960-2

RESULT 11

Query Match Similarity 100.0%; Score 27; DB 15; Length 173;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 165 RTRGG 169

RESULT 13
 US-10-260-562-2
 ; Sequence 2, Application US/10-260-562
 ; Publication No. US20030096320A1
 ; GENERAL INFORMATION
 ; APPLICANT: Moloney, Maurice
 ; APPLICANT: Boothe, Joseph
 ; APPLICANT: Roolien, Gijs van
 ; TITLE OF INVENTION: Oil Bodies and Associated Proteins as Affinity Matrices
 ; FILE REFERENCE: 9369-239
 ; CURRENT APPLICATION NUMBER: US/10-260,562
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: US 09/319,275
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: US 08/767,026
 ; PRIOR FILING DATE: 1997-12-16
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis Thaliana
 ; US-10-260-562-2

Query Match Similarity 100.0%; Score 27; DB 15; Length 173;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 165 RTRGG 169

RESULT 14
 US-09-893-525-5
 ; Sequence 5, Application US/09893525
 ; Publication No. US20030126631A1
 ; GENERAL INFORMATION
 ; APPLICANT: Moloney, Maurice M.
 ; APPLICANT: Van Roolien, Gijs
 ; TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodies
 ; CURRENT APPLICATION NUMBER: US/09/893,525
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 09/210,843
 ; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: US 08/846,021
 ; PRIOR APPLICATION NUMBER: US 08/7366,783
 ; PRIOR FILING DATE: 1994-12-30
 ; PRIOR APPLICATION NUMBER: US 08/142,418
 ; PRIOR FILING DATE: 1993-11-16
 ; PRIOR APPLICATION NUMBER: US 07/659,835
 ; PRIOR FILING DATE: 1991-02-22
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 5
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: Brassica napus
 ; US-09-893-525-5

Query Match Similarity 100.0%; Score 27; DB 11; Length 187;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 ; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; Qy 1 RTRGG 5
 ; Db 179 RTRGG 183

RESULT 15
 US-09-910-562-4
 ; Sequence 4, Application US/09910562
 ; Patent No. US20030098163A1
 ; GENERAL INFORMATION
 ; APPLICANT: Zeng et al.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptors TR21 and TR22
 ; FILE REFERENCE: RF530
 ; CURRENT APPLICATION NUMBER: US/09/910,562
 ; CURRENT FILING DATE: 2001-07-23
 ; PRIOR APPLICATION NUMBER: 60/221,143
 ; PRIOR FILING DATE: 2000-07-27
 ; PRIOR APPLICATION NUMBER: 60/220,116
 ; PRIOR FILING DATE: 2000-07-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-910-562-4

Query Match Similarity 100.0%; Score 27; DB 9; Length 194;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 1 RTRGG 5

Search completed: September 9, 2003, 23:47:28
 Job time : 47.875 secs

Query Match Similarity 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 RTRGG 8

RESULT 4
US 10-287-043-2188
; Sequence 2188, Application US/10287043
; GENERAL INFORMATION:
; APPLICANT: Proteon Ltd
; APPLICANT: Higher eukaryote patent
; FILE REFERENCE: Higher eukaryote patent
; CURRENT APPLICATION NUMBER: US/10/287,043
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 3214
; SOFTWARE: Protpatent version 1.0
SEQ ID NO 2188
LENGTH: 10

TYPE: PRT
ORGANISM: Saccharomyces cerevisiae

OTHER INFORMATION: Sequence located in YPL119C at 549-558 and may interact with § 10-287-043-2188

Query Match Similarity 100.0%; Score 27; DB 28; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5

Db 5 RTRGG 9

RESULT 5
US-08-222-626A-41
; Sequence 41, Application US/08222626A
; GENERAL INFORMATION:
; APPLICANT: Arai, Naoko
; APPLICANT: Tokumitsu, Hiroshi
; APPLICANT: Esteban, S.
; TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
; TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,626A
FILING DATE: 04-APR-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/148,061
FILING DATE: 05-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/113,971
FILING DATE: 30-AUG-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/088,998
FILING DATE: 30-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/088,483
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.

RESULT 3
US-10-287-043-2186
; Sequence 2186, Application US/10287043
; GENERAL INFORMATION:
; APPLICANT: Proteon Ltd
; TITLE OF INVENTION: Complementary peptide ligands from higher eukaryote genome sequer
; FILE REFERENCE: Higher eukaryote parent
; CURRENT APPLICATION NUMBER: US/10/287,043
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 3214
; SOFTWARE: Protpatent version 1.0
SEQ ID NO 2186
LENGTH: 10

TYPE: PRT
ORGANISM: Saccharomyces cerevisiae

FEATURE:
OTHER INFORMATION: Sequence located in YPL119C at 550-559 and may interact with seq US-10-287-043-2186

Query Match Similarity 100.0%; Score 27; DB 28; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5

REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0392K3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-222-626A-41

Query Match, Best Local Similarity 100.0%; Score 27; DB 6; Length 19; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5

Db 2 RTRGG 6

Query Match, Best Local Similarity 100.0%; Score 27; DB 6; Length 19; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5

Db 2 RTRGG 6

SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-009-843C-150

SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-009-843C-150

Query Match, Best Local Similarity 100.0%; Score 27; DB 14; Length 19; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5

Db 2 RTRGG 6

Query Match, Best Local Similarity 100.0%; Score 27; DB 14; Length 19; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5

Db 2 RTRGG 6

RESULT 5
 US-01-009-843C-150
 Sequence 150, Application US/09009843C

GENERAL INFORMATION:
 APPLICANT: Arai, Naoko
 APPLICANT: Masuda, Esteban S.
 APPLICANT: Tokumitsu, Hiroshi
 TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN
 TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS
 NUMBER OF SEQUENCES: 266
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30; #2.0; and
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/009, 843C
 FILING DATE: 20-JAN-1998
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/222, 626
 FILING DATE: 04-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/148, 061
 FILING DATE: 05-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/113, 971
 FILING DATE: 30-AUG-1993
 APPLICATION NUMBER: US 08/099, 998
 FILING DATE: 04-APR-1994
 APPLICATION NUMBER: US 08/148, 061
 FILING DATE: 05-NOV-1993
 APPLICATION NUMBER: US 08/113, 971
 FILING DATE: 30-AUG-1993
 APPLICATION NUMBER: US 08/099, 998
 FILING DATE: 30-JUL-1993
 APPLICATION NUMBER: US 08/088, 483
 FILING DATE: 06-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0392K3B

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-852-9196
 TELEFAX: 650-496-1200
 INFORMATION FOR SEQ ID NO: 150:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 MOLECULE DESCRIPTION: SEQ ID NO: 150:
 US-09-009-843D-150

SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 MOLECULE DESCRIPTION: SEQ ID NO: 150:
 US-09-009-843D-150

Query Match, Best Local Similarity 100.0%; Score 27; DB 14; Length 19;

Qy 100.0%; Score 27; DB 14; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTRGG 5 Db 2 RTRGG 6

RESULT 8

PCT-US00-26524B-6856

Sequence 6856, Application PC/TUS0026524B

GENERAL INFORMATION:

APPLICANT: Birs et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005PCT

CURRENT APPLICATION NUMBER: PCT/US00/26524B

CURRENT FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6856

LENGTH: 32

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (17)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (22)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (23)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (23)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (25)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (25)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (25)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

PCT-US00-26524B-6856

Query Match 100.0%; Score 27; DB 1; Length 32; Best Local Similarity 100.0%; Pred. No. 6e+02; Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTRGG 5 Db 26 RTRGG 30

RESULT 9

US-09-270-767-58721

Sequence 58721, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62317

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58721

LENGTH: 33

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-58721

Query Match 100.0%; Score 27; DB 16; Length 33; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTRGG 5 Db 9 RTRGG 13

RESULT 10

US-09-270-849B-185516

Sequence 185516, Application US/09270849B

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,688

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PatentIn Ver. 3.0

SEQ ID NO 6866

LENGTH: 32

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-270-849B-185516

Query Match 100.0%; Score 27; DB 16; Length 33; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTRGG 5

Db 9 RTRGG 13

RESULT 12

US-09-617-682A-3655

GENERAL INFORMATION:

APPLICANT: BROVER, Wrzeseslaw

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

FILE REFERENCE: 2750-1053

CURRENT APPLICATION NUMBER: US/09/617,682A

CURRENT FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 16871

SEQ ID NO 3655

LENGTH: 34

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..34

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..34

OTHER INFORMATION: Ceres Seq. ID 1351169

US-09-617-682A-3655

RESULT 13

Sequence 37, Application US/0894853BA

GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GRANDOS, EDWARD N.

APPLICANT: KLAAS, MICHAEL R.

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.

APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL ASPARTYL PROTEASE

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING AND

TITLE OF INVENTION: TREATING DISEASES OF THE LUNG

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,538A

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

PRATOR APPLICATION NUMBER:

FILING DATE:

Query Match 100.0%; Score 27; DB 20; Length 34;

Best Local Similarity 100.0%; Pred. No. 6.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

Db 7 RTRGG 11

Qy 1 RTRGG 5

Db 18 RTRGG 22

RESULT 14

PC/US01-14827-12097

Sequence 12097, Application PC/US0114827

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 21272-104

CURRENT APPLICATION NUMBER: PCT/US01/14827

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 09/577,408

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 16102

SOFTWARE: Custom

SEQ ID NO 12097

LENGTH: 37

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US01-14827-12097

Query Match 100.0%; Score 27; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

Db 3 RTRGG 7

Qy 1 RTRGG 5

Db 3 RTRGG 7

RESULT 15

PC/US01-01354-9822

Sequence 9822, Application PC/US0101354

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc. et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: FC004/PCT

CURRENT APPLICATION NUMBER: PCT/US01/01354

CURRENT FILING DATE: 2001-03-17

NUMBER OF SEQ ID NOS: 42506

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9822

LENGTH: 41

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US01-01354-9822

Query Match 100.0%; Score 27; DB 1; Length 41;

Best Local Similarity 100.0%; Pred. No. 7.7e+02;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	RTRGG	5						
Db	19	RTRGG	23						

Search completed: September 9, 2003, 23:45:44
Job time : 356 secs

Copyright (c) 1993 - 2003 Compugen Ltd. GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2003, 23:32:23 ; Search time 10.625 Seconds

Perfect score: 27 (without alignments)

Sequence: 4.496 Million cell updates/sec

Title: US-09-967-003-3

Scoring table: BLOSUM62

Searched: Gapext 0.5

1 RTKGG 5

Total number of hits satisfying chosen parameters: 47124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New:*

1: /rcgn2_6/ptodata/1/paa/US06_NEWCOMB.pep:*

2: /rcgn2_6/ptodata/1/paa/US06_NEWCOMB.pep:*

3: /rcgn2_6/ptodata/1/paa/US07_NEWCOMB.pep:*

4: /rcgn2_6/ptodata/1/paa/US08_NEWCOMB.pep:*

5: /rcgn2_6/ptodata/1/paa/US09_NEWCOMB.pep:*

6: /rcgn2_5/ptodata/1/paa/US10_NEWCOMB.pep:*

7: /rcgn2_6/ptodata/1/paa/US60_NEWCOMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	27	100.0	277 5	US-09-674-576A-1227 Sequence 1227
2	27	100.0	537 1	PCT-US03-24505-26 Sequence 26, P
3	27	100.0	537 1	US-60-855-150-1577 Sequence 1577
4	24	88.9	149 7	US-60-955-114-1990 Sequence 1690
5	24	88.9	550 5	US-09-581-286A-499 Sequence 499,
6	24	88.9	599 5	US-09-581-286A-499 Sequence 498,
7	24	88.9	614 5	US-09-581-286A-364 Sequence 364,
8	24	88.9	835 7	US-60-490-880-896 Sequence 896,
9	24	88.9	2705 1	PCT-US03-25150-97 Sequence 97, P
10	23	85.2	26 5	US-09-592-617C-4 Sequence 4, P
11	23	85.2	27 5	US-09-592-617C-38 Sequence 38, P
12	23	85.2	193 7	US-60-900-820-1318 Sequence 1518
13	23	85.2	194 7	US-60-487-610-656 Sequence 1565
14	23	85.2	235 1	PCT-US02-25560R-337 Sequence 337,
15	23	85.2	311 1	PCT-US02-29560A-338 Sequence 338,
16	23	85.2	321 5	US-09-897-516A-6988 Sequence 6988
17	23	85.2	402 6	US-09-897-211-870-46 Sequence 46,
18	23	85.2	402 6	US-10-650-67-46 Sequence 46,
19	23	85.2	420 7	US-60-678-777-12 Sequence 12,
20	23	85.2	443 7	US-60-678-777-10 Sequence 10, P
21	23	85.2	471 5	US-09-897-316A-7981 Sequence 7981,
22	23	85.2	495 5	US-09-976-858-177 Sequence 177,
23	23	85.2	669 7	US-60-885-0-1584 Sequence 1584
24	23	85.2	707 7	US-60-485-450-1585 Sequence 1585,
25	23	85.2	748 7	US-60-487-610-6529 Sequence 2629,
26	23	85.2	748 7	US-60-495-114-2124 Sequence 2124,

RESULT 1
 US-09-674-546A-1227
 Sequence 1227, Application US/09674546A
 GENERAL INFORMATION:
 APPLICANT: Institute for Genomic Research
 APPLICANT: Chiron Corporation
 TITLE OF INVENTION: *Neisseria Meningitidis* Antigens and Compositions
 FILE REFERENCE: CHIR-0334
 CURRENT APPLICATION NUMBER: US/09-674,546A
 CURRENT FILING DATE: 1999-04-30
 NUMBER OF SEQ ID NOS: 3264
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 1227
 LENGTH: 277
 TYPE: PRT
 ORGANISM: *Neisseria meningitidis*
 US-09-674-546A-1227

RESULT 2
 PCT-US03-24505-26
 Sequence 26, Application PC/TUS0324505
 GENERAL INFORMATION:
 APPLICANT: EXELIXIS, INC.
 TITLE OF INVENTION: MP2155S AS MODIFIERS OF THE P21 OR P53 PATHWAY AND METHODS OF
 FILE REFERENCE: EX03-055C-PC
 CURRENT APPLICATION NUMBER: PCT/US03/24505
 CURRENT FILING DATE: 2003-08-06
 PRIOR APPLICATION NUMBER: US 60/401,701
 PRIOR FILING DATE: 2002-08-07
 PRIOR APPLICATION NUMBER: US 60/411,017
 PRIOR FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: US 60/437,107
 PRIOR FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 26
 LENGTH: 537
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 PCT-US03-24505-26

ALIGNMENTS

Sequence 2125, AP
 Sequence 6173, AP
 Sequence 2367, AP
 Sequence 1484, AP
 Sequence 2725, AP
 Sequence 2, Appl1
 Sequence 1574, AP
 Sequence 43, Appl1
 Sequence 4, Appl1
 Sequence 1850, AP
 Sequence 1848, AP
 Sequence 1851, AP
 Sequence 1852, AP
 Sequence 1849, AP
 Sequence 1849, AP
 Sequence 958, AP
 Sequence 117, AP
 Sequence 122, AP

Query Match 100.0%; Score 27; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 77 RTRGG 81

RESULT 3
US-60-485-450-1577
; Sequence 1577, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGIL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1577
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-485-450-1577

Query Match 100.0%; Score 27; DB 7; Length 537;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 77 RTRGG 81

RESULT 4
US-60-495-114-1690
; Sequence 1690, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGIL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001480
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SEQ ID NO 1690
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-495-114-1690

Query Match 88.9%; Score 24; DB 7; Length 149;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 126 KTRGG 130

RESULT 5
US-09-581-286A-499
; Sequence 499, Application US/09581286A
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; APPLICANT: BARR, IAN G.
; APPLICANT: PATTERSON, MICHELLE A.
; APPLICANT: AGIUS, CATHERINE T.
; APPLICANT: ROTHEL, LINDA J.
; APPLICANT: MARKETTS, MAL B.
; APPLICANT: HOCKING, DIANNA M.
; APPLICANT: WEBB, ELIZABETH A.
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
; FILE REFERENCE: 4137-3
; CURRENT APPLICATION NUMBER: US/09/581,286A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 499
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-581-286A-499

RESULT 6
US-09-581-286A-498
; Sequence 498, Application US/09581286A
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; APPLICANT: BARR, IAN G.
; APPLICANT: PATTERSON, MICHELLE A.
; APPLICANT: AGIUS, CATHERINE T.
; APPLICANT: ROTHEL, LINDA J.
; APPLICANT: MARKETTS, MAL B.
; APPLICANT: HOCKING, DIANNA M.
; APPLICANT: WEBB, ELIZABETH A.
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
; FILE REFERENCE: 4137-3
; CURRENT APPLICATION NUMBER: US/09/581,286A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 498
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-581-286A-498

Query Match 88.9%; Score 24; DB 5; Length 550;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 88 RTRGG 92

RESULT 7
US-09-581-286A-499
; Sequence 499, Application US/09581286A
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; APPLICANT: BARR, IAN G.
; APPLICANT: PATTERSON, MICHELLE A.
; APPLICANT: AGIUS, CATHERINE T.
; APPLICANT: ROTHEL, LINDA J.
; APPLICANT: MARKETTS, MAL B.
; APPLICANT: HOCKING, DIANNA M.
; APPLICANT: WEBB, ELIZABETH A.
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
; FILE REFERENCE: 4137-3
; CURRENT APPLICATION NUMBER: US/09/581,286A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 499
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-581-286A-499

Query Match 88.9%; Score 24; DB 7; Length 550;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 126 KTRGG 130

RESULT 8
US-09-581-286A-499
; Sequence 499, Application US/09581286A
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; APPLICANT: BARR, IAN G.
; APPLICANT: PATTERSON, MICHELLE A.
; APPLICANT: AGIUS, CATHERINE T.
; APPLICANT: ROTHEL, LINDA J.
; APPLICANT: MARKETTS, MAL B.
; APPLICANT: HOCKING, DIANNA M.
; APPLICANT: WEBB, ELIZABETH A.
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
; FILE REFERENCE: 4137-3
; CURRENT APPLICATION NUMBER: US/09/581,286A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 499
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
; US-09-581-286A-499

Query Match 88.9%; Score 24; DB 7; Length 550;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
Db 126 KTRGG 130

RESULT 9
US-09-581-286A-499
; Sequence 499, Application US/09581286A
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.

PRIOR APPLICATION NUMBER: AU PP 2264
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: AU PP 2911
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: AU PP 3128
 PRIOR FILING DATE: 1998-04-23
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: AU PP 3338
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: AU PP 4917
 PRIOR FILING DATE: 1998-07-29
 Remaining prior application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 498
 LENGTH: 599
 TYPE: PRT
 ORGANISM: *Porphyromonas gingivalis*
 US-09-581-286A-498

Query Match 88.9%; Score 24; DB 5; Length 599;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 152 RTRGG 156

RESULT 7
 US-09-581-286A-364
 Sequence 364, Application US/09581286A
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSS, BRUCE C.
 ; APPLICANT: BARR, IAN G.
 ; APPLICANT: PATTERSON, MICHELLE A.
 ; APPLICANT: AGIUS, CATHERINE T.
 ; APPLICANT: ROTHERL, LINDA J.
 ; APPLICANT: MARGENTIS, MAL B.
 ; APPLICANT: HOCKING, DIANNA M.
 ; APPLICANT: WEBB, ELIZABETH A.
 TITLE OF INVENTION: *PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES*
 FILE REFERENCE: 4137-3
 CURRENT APPLICATION NUMBER: US/09/581,286A
 CURRENT FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: PCT/AU98/01023
 PRIOR FILING DATE: 1998-12-10
 PRIOR APPLICATION NUMBER: AU PP 0839
 PRIOR FILING DATE: 1997-12-10
 PRIOR APPLICATION NUMBER: AU PP 1182
 PRIOR FILING DATE: 1997-12-31
 PRIOR APPLICATION NUMBER: AU PP 1846
 PRIOR FILING DATE: 1998-01-30
 PRIOR APPLICATION NUMBER: AU PP 2264
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: AU PP 2911
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: AU PP 3128
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: AU PP 3338
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: AU PP 3654
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: AU PP 4917
 PRIOR FILING DATE: 1998-07-29
 Remaining prior application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 721
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 364
 LENGTH: 614
 TYPE: PRT
 ORGANISM: *Porphyromonas gingivalis*

RESULT 8
 US-60-490-890-896
 Sequence 896, Application US/60490890
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Martin
 ; APPLICANT: Rupnow, Brent A.
 ; APPLICANT: Webster, Kevin R.
 ; APPLICANT: Jackson, Donald
 ; APPLICANT: Wong, Tai W.
 TITLE OF INVENTION: *BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION*
 FILE REFERENCE: D0310 PSP
 CURRENT APPLICATION NUMBER: US/60/490,890
 CURRENT FILING DATE: 2003-07-29
 NUMBER OF SEQ ID NOS: 2779
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 896
 LENGTH: 835
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 US-60-490-890-896

Query Match 88.9%; Score 24; DB 7; Length 835;
 Best Local Similarity 80.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 825 KTRGG 829

RESULT 9
 PCT-US03-21510-97
 Sequence 97, Application PC/US0321510
 ; GENERAL INFORMATION:
 ; APPLICANT: EXELIXIS, INC.
 TITLE OF INVENTION: *MAP215 AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE*
 FILE REFERENCE: EX03-046C-PC
 CURRENT APPLICATION NUMBER: PCT/US03/21510
 CURRENT FILING DATE: 2003-07-09
 PRIOR APPLICATION NUMBER: US 60/394,795
 PRIOR FILING DATE: 2002-07-10
 PRIOR APPLICATION NUMBER: US 60/401,739
 PRIOR FILING DATE: 2002-08-07
 PRIOR APPLICATION NUMBER: US 60/411,010
 PRIOR FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: US 60/437,158
 PRIOR FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 97
 LENGTH: 2705
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 PCT-US03-21510-97

Query Match 88.9%; Score 24; DB 1; Length 2705;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RTRGG 5
 Db 2175 KTRGG 2179

RESULT 10
US-09-592-617C-4
; Sequence 4, Application US/09592617C
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT APPLICATION NUMBER: US/09/592,617C
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/7380, 167
; PRIOR FILING DATE: 1999-01-30
; PRIOR APPLICATION NUMBER: US 08/2116, 081
; PRIOR FILING DATE: 1994-03-21
; PRIOR APPLICATION NUMBER: US 07/637, 830
; PRIOR FILING DATE: 1991-01-04
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-592-617C-4

Query Match 85.2%; Score 23; DB 5; Length 26;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTRGG 5
Db 3 QTRGG 7

RESULT 11
US-09-592-617C-38
; Sequence 38, Application US/09592617C
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M. Armin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
; FILE REFERENCE: 00786-267002
; CURRENT APPLICATION NUMBER: US/09/592,617C
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 08/380, 167
; PRIOR FILING DATE: 1999-01-10
; PRIOR APPLICATION NUMBER: US 08/2116, 081
; PRIOR FILING DATE: 1994-03-21
; PRIOR APPLICATION NUMBER: US 07/637, 830
; PRIOR FILING DATE: 1991-01-04
; PRIOR APPLICATION NUMBER: US 07/539, 842
; PRIOR FILING DATE: 1990-06-18
; PRIOR APPLICATION NUMBER: US 07/212, 573
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-592-617C-38

Query Match 85.2%; Score 23; DB 5; Length 27;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTRGG 5
Db 4 QTRGG 8

RESULT 12
US 60-490-890-1518
; Sequence 1518, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1518
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-1518

Query Match 85.2%; Score 23; DB 7; Length 193;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTRGG 5
Db 4 RSRGG 8

RESULT 13
US 60-487-610-1656
; Sequence 1656, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CLO0469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1656
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1656

Query Match 85.2%; Score 23; DB 7; Length 194;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTRGG 5
Db 131 QTRGG 135

RESULT 14
PCT-US02-295560A-337
; Sequence 337, Application PC/US02295560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezsi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560A
CURRENT FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: US 60/323,469

PRIOR FILING DATE: 2001-09-17

NUMBER OF SEQ ID NOS: 412

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 337

LENGTH: 235

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US02-29560A-337

Query Match 85.2%; Score 23; DB 1; Length 235;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTRGG 5
Db 162 QTRGG 166

RESULT 15

PCT-US02-29560A-338

Sequence 338, Application PCT/US02/29560A

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Ariz, Natasha

APPLICANT: Gish, Kurt C.

APPLICANT: Hevezsi, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Wilson, Keith E.

APPLICANT: Zlotnik, Albert

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501-002710PC

CURRENT APPLICATION NUMBER: PCT/US02/29560A

CURRENT FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: US 60/323,469

PRIOR FILING DATE: 2001-09-17

NUMBER OF SEQ ID NOS: 412

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 338

LENGTH: 311

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US02-29560A-338

Query Match 85.2%; Score 23; DB 1; Length 311;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTRGG 5
Db 238 QTRGG 242

Search completed: September 9, 2003, 23:46:06

Job time : 11.625 secs

A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:
 A;Gene: ytfp

Query Match 100.0%; Score 27; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 70 RTRGG 74

RESULT 3

H91278 hypothetical protein ECsf200 [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001
 C;Accession: H91278

R;Bayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA, Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gene
 A;Reference number: A99629; MOLID:21156231; PMID:11258796
 A;Accession: H91278
 A;Molecule type: DNA
 A;Residues: 1-113 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA038623:1; PID:913364677; GSPDB:GN00154
 A;Experimental source: strain 0157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: ECsf200

Query Match 100.0%; Score 27; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 70 RTRGG 74

RESULT 4

H86119 hypothetical protein ytfp [imported] - Escherichia coli (strain 0157:H7, substrain EDL93)
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: H86119
 R;Perna, N.T.; Plunkett III, G.; Burriand, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Bacteriol. 179, 7135-7155, 1997
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
 A;Reference number: A85480; MOLID:21074935; PMID:1120551
 A;Accession: H86119
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-113 <STO>
 A;Cross-references: GB:AP0005174; NID:912519221; PIDN:AG59420:1; GSPDB:GN00145; UWGP:258
 A;Experimental source: strain 0157:H7, substrain EDL93
 C;Genetics:
 A;Gene: ytfp

Query Match 100.0%; Score 27; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 70 RTRGG 74

RESULT 5

A64384 ribosomal protein S8-eR - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: A64384
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blakemore, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, J.D.; Sadow, P.W.; Hana, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese C;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MOLID:95337999; PMID:8688087

RESULT 6

D69125 ribosomal protein S8 - Methanobacterium thermoautotrophicum (strain Delta H)
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 13-Aug-1999
 C;Accession: D69125
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oiu, D.; Spadafora, R.; Vicare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, T.; Oiu, D.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.; Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A;Reference number: A69000; MOLID:98037514; PMID:9371463
 A;Accession: D69125
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-127 <MPH>
 A;Cross-references: GB:AE000807; GB:AE000666; NID:92621239; PIDN:AA84713:1; PID:9262
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MH207
 C;Superfamily: rat ribosomal protein S8

Query Match 100.0%; Score 27; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 46 RTRGG 50

RESULT 7

A64384 ribosomal protein S8-eR - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: A64384
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blakemore, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, J.D.; Sadow, P.W.; Hana, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese C;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MOLID:95337999; PMID:8688087

A;Accession: A64384
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Residues: 1-129 <BUL>
 A;Cross-references: GB:U67514; GB:L77117; NID:92826304; PIDN:AB98667.1; PID:g1591387; T
 A;Genetics:
 A;Map position: R0599257-599646
 C;Superfamily: rat ribosomal protein S8
 C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 27; DB 2; length 129;
 Best Local Similarity 100.0%; Pred. No. 55; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 48 RTRGG 52

RESULT 8
 E81222 hypothetical protein NMB0247 [imported] - *Neisseria meningitidis* (strain MC58 serogroup C;Species: *Neisseria meningitidis*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C;Accession: E81222
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R.; Hickie, E.K.; Haft, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Socrato, V.; Massignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Wei, A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-145 <TER>
 A;Cross-references: GB:AE002381; GB:AE002098; NID:97225455; PIDN:AAF40701.1; PID:9722546
 C;Experimental source: serogroup B, strain MC58
 C;Genetics:
 C;Gene: NMB0247
 C;Superfamily: *Neisseria meningitidis* hypothetical protein NMB0247

Query Match 100.0%; Score 27; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 61; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 91 RTRGG 95

RESULT 9
 A81992 hypothetical protein NMB0013 [imported] - *Neisseria meningitidis* (strain 22491 serogroup C;Species: *Neisseria meningitidis*
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C;Accession: A81992
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Bolard, S.; Jäger, K.; Leather, S.; Moulis, S.; Mungall, K.; Quail, M.A.; Rajandream, A;Nature 404, 502-505, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-145 <PAR>
 A;Cross-references: GB:U1162752; GB:U1157959; NID:97378778; PIDN:CAB8333.1; PID:9737879
 A;Experimental source: serogroup A, strain 22491
 C;Genetics:
 C;Gene: NMB0013
 C;Superfamily: *Neisseria meningitidis* hypothetical protein NMB0247

Query Match 100.0%; Score 27; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 61; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 S22538 oleosin, 18.5K - *Arabidopsis thaliana*
 N;Alternate names: protein F13M3.280
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: S22538; T05535; S22143
 R;van Rooijen, G.J.H.; Terning, L.I.; Moloney, M.M.
 A;Title: Nucleotide sequence of an *Arabidopsis thaliana* oleosin gene.
 A;Reference number: S22538; MUID:92288310; PMID:1600152
 A;Accession: S22538
 A;Molecule type: DNA
 A;Residues: 1-173 <R00>
 A;Cross-references: EMBL:X62353; NID:916404; PIDN:CAA44225.1; PID:916405
 A;Experimental source: cv. Columbia
 R;Bevan, M.; Wedder, H.; Wedder, E.; Wanburt, R.; Hobeissel, J.; Mewes, H.W.; Mayer, A;Reference number: Z15419
 A;Accession: T05535
 A;Molecule type: DNA
 A;Residues: 1-173 <BEV>
 A;Cross-references: EMBL:AL035523
 A;Experimental source: cultivar Columbia; BAC clone F13M23
 C;Genetics:
 A;Map position: 4
 A;Introns: 118/2
 A;Note: F13M23-280
 C;Superfamily: oleosin
 C;Keywords: seed

Query Match 100.0%; Score 27; DB 1; Length 173;
 Best Local Similarity 100.0%; Pred. No. 72; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTRGG 5
 Db 165 RTRGG 169

RESULT 11
 VCVOB3 coat protein - barley yellow dwarf virus (strain MAV-PS1)
 C;Species: barley yellow dwarf virus, BYDV
 C;Accession: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jun-2000
 R;Ueng, P.P.; Vincent, J.R.; Kawata, E.E.; Lei, C.H.; Lister, R.M.; Larkins, B.A.
 J;Gen. Virol. 73, 487-492, 1992
 A;Title: Nucleotide sequence analysis of the genomes of the MAV-PS1 and P-PAV isolat
 A;Reference number: J01409; MUID:92166764; PMID:1538199
 A;Accession: J01411
 A;Molecule type: genomic RNA
 A;Residues: 1-199 <UER>
 A;Cross-references: GB:U11028; DDBJ:U01213; NID:9211084; PIDN:BA01781.1; PID:922108
 C;Superfamily: potato leaf roll virus coat protein; potato leaf roll virus coat prot
 F;1-199/domain: potato leaf roll virus coat protein homology <COP>
 Query Match 100.0%; Score 27; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 82; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C;Keywords: coat protein

Qy 1 RTRGG 5
 Db 44 RTRGG 48

RESULT 12	
A; Accession: R0986	coat protein - barley yellow dwarf virus (isolate MAV)
A; Molecule type: DNA	
A; Residues: 70-200 <B00>	
A; Cross-references: EMBL:J05637; NID:9171726; PIDN:AAA63573.1; PID:9171727	
N; Alternate names: capsid protein	
C; Species: barley yellow dwarf virus, BYDV	
C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 20-Sep-1999	
C; Accession: S10986	
R; Rizzo, T.M.; Gray, S.M.	
Nucleic Acids Res. 18, 625, 1990	
A; Title: Cloning and sequence analysis of a cDNA encoding the capsid protein of the MAV	
A; Reference number: S10986; MUID:90356431; PMID:2388853	
C; Superfamily: potato leaf roll virus coat protein	
A; Accession: S10986	
A; Molecule type: genomic RNA	
A; Residues: 1-199 <R12>	
A; Cross-references: EMBL:X33174; NID:960519; PIDN:CAA37315.1; PID:960520	
A; Molecule type: coat protein	
C; Superfamily: potato leaf roll virus coat protein	
F; 1199/Domain: potato leaf roll virus coat protein homology <COP>	
Query Match 100.0%; Score 27; DB 2; Length 199;	
Best Local Similarity 100.0%; Pred. No. 82; Mismatches 0; Indels 0; Gaps 0;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 RTRGG 5	
Db 44 RTRGG 48	
RESULT 13	
S45591	
ribosomal protein s8.e, cytosolic - yeast (<i>Saccharomyces cerevisiae</i>)	
A; Species: <i>Saccharomyces cerevisiae</i>	
C; Date: 19-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 23-Mar-2001	
C; Accession: S45591; S50808; S20605; S11250; A66590; S30421	
R; Logge, M.; Moelmans, F.; Fiers, W.; Contreras, R.	
Yeast 10, 1093-1100, 1994	
A; Title: The two genes encoding yeast ribosomal protein S8 reside on different chromosomes	
A; Residues: 1-5588; MUID:9084636; PMID:792509	
A; Accession: S45591	
A; Molecule type: DNA	
A; Residues: 1-200 <LOG>	
A; Cross-references: EMBL:Z226879; NID:9407519; PIDN:CAA81525.1; PID:9407523	
A; Reference number: S45802	
R; Contreras, R.; Fiers, W.; Logge, M.; Moelmans, F.	
submitted to the Protein Sequence Database, August 1994	
A; Residues: 1-200 <CON>	
A; Cross-references: EMBL:Z35833; GSPDB:GN00002; MIPS:YBL072c; NID:9536114; PIDN:CAA84893	
A; Genetics: CH2	
R; Dierckx, P.S.	
submitted to the EMBL Data Library, December 1994	
A; Description: The sequence of <i>S. cerevisiae</i> cosmids 9747, 8198, 9781, and lambda clones	
A; Accession: S50436	
A; Reference number: S50436	
A; Molecule type: DNA	
A; Residues: 1-200 <DIE>	
A; Cross-references: EMBL:U18839; NID:903313; PIDN:AAB64657.1; PID:9603340; GSPDB:GN00002	
A; Genetics: CH5	
R; Ootaka, E.; Higo, K.I.; Itoh, T.	
Mol. Gen. Genet. 195, 544-546, 1984	
A; Title: Yeast ribosomal proteins. VIII. Isolation of two proteins and sequence character	
A; Reference number: S11249	
A; Accession: S11250	
A; Molecule type: protein	
A; Residues: 2-5, 'B', 7-19, 'Z', 21-27, 'Z', 29-31, 'Z', 33-34, 'B', 36-48, 'K', 50-51 <C7A>	
R; Boerstler, W.R.; Craig, E.A.	
J. Biol. Chem. 265, 18912-18921, 1990	
A; Title: Structure and regulation of the SSA4 HSP70 gene of <i>Saccharomyces cerevisiae</i> .	
A; Reference number: A66590; MUID:91035412; PMID:2121731	
Qy 1 RTRGG 5	
Db 47 RTRGG 51	
RESULT 14	
T49000	
probable ribosomal protein Rps8bp [Imported] - <i>Neurospora crassa</i>	
N; Alternate names: protein Bl1B22.20	
C; Species: <i>Neurospora crassa</i>	
C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000	
C; Accession: T49000	
R; Shulke, U.; Alig, V.; Hoheisel, J.; Brandt, P.; Furtmann, B.; Holland, R.; Nyakatu	
submitted to the Protein Sequence Database, May 2000	
A; Reference number: 225022	
A; Accession: T49800	
A; Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-202 <SCH>	
A; Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:Bl1B22.20	
A; Experimental source: BAC clone Bl1B22; strain OR74A	
C; Genetics:	
A; Gene: NCSP:Bl1B22.20	
A; MPP position: 6	
A; Introns: 19/2; 83/1	
C; Superfamily: rat ribosomal protein S8	
Query Match 100.0%; Score 27; DB 2; Length 202;	
Best Local Similarity 100.0%; Pred. No. 83; Mismatches 0; Indels 0; Gaps 0;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 RTRGG 5	
Db 47 RTRGG 51	
RESULT 15	
T16343	
hypothetical protein F42C5.8 - <i>Caenorhabditis elegans</i>	
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999	
C; Accession: T16343	
R; D1, Z	
submitted to the EMBL Data Library, November 1995	
A; Description: The sequence of <i>C. elegans</i> cosmid F42C5.	
A; Reference number: Z18497	
A; Accession: T16343	
A; Status: preliminary; translated from GB/EMBL/DDJB	
A; Molecule Type: DNA	
A; Residues: 1-208 <D0Z>	
A; Cross-references: EMBL:U40799; NID:91065935; PID:91065942; PIDN:AAA81485.1; CESP:F4	
C; Genetics:	
A; Gene: CESP:F42C5.8	

A; Introns: 37/3; 71/1; 173/1
C; Superfamily: rat ribosomal protein s8

Query Match 100.0%; Score 27; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0;
Qy 1 RTRGG 5
Db 47 RTRGG 51
|||||

Search completed: September 9, 2003, 23:35:23
Job time : 33.25 secs

Scoring table: BLOSUM62									
Gapop 10.0 , Gapext 0.5									
Searched: 127863 seqs, 47026705 residues									
Total number of hits satisfying chosen parameters: 127863									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database : SwissProt; 41;*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
1	27	100.0	113	1	YTFP_ECOLI	YTFP_ECOLI	RESULT 1	113 AA.	
2	27	100.0	127	1	RSBE_METTH	P39223 escherichia	ID		
3	27	100.0	129	1	RSBE_METTH	024309 methanobact	AC		
4	27	100.0	173	1	OLEL_ARATH	P50055 methanococc	P3323;		
5	27	100.0	199	1	COAT_BID1	P29525 arabidopsis	01-FEB-1995 (Rel. 31, Last sequence update)		
6	27	100.0	199	1	COAT_BYDM	Q00010 barley yell	DT		
7	27	100.0	199	1	RSB_YEAST	P17966 barley yell	28-FEB-2003 (Rel. 41, Last annotation update)		
8	27	100.0	208	1	RSB_CAEFF	P07554 saccharomyce	DE		
9	27	100.0	299	1	SP4_HUMAN	P81556 caenorhabdi	HYPOTHETICAL protein YTFP		
10	27	100.0	310	1	Y942_SUSCO	P96044 homo sapien	YTFP OR B422 OR C5320 OR Z5833 OR EC55200 OR SF4265.		
11	27	100.0	313	1	CBRL_RHIME	Q97zh1 sulfobolus	NCBI_TaxID=562, 217992, 83334, 623;		
12	27	100.0	313	1	CBR2_RHIME	P8332 rhizobium m	[1]		
13	27	100.0	316	1	LDB_BOBR	P5688 rhizobium m	SEQUENCE FROM N. A.		
14	27	100.0	349	1	VPT_AHSV6	P93052 botryococcus	SPECIES=E.coli; STRAIN=K12 / MG1655;		
15	27	100.0	349	1	VPT_AHSV9	P70127 african hor	MEDLINE=95-334362; PubMed=7610040;		
16	27	100.0	350	1	VPT_AHSV4	P36325 african hor	Blattner F.R., Plunkett G. III, Sofia H.J., Daniels D.L.,		
17	27	100.0	379	1	PSI_SCHEO	P009912 schizosacch	RX		
18	27	100.0	533	1	ALG6_ARATH	009f17 arabidopsis	RX		
19	27	100.0	533	1	YIN_CHICK	Q05876 gallus gallus	MEDLINE=22388234; PubMed=1247157;		
20	27	100.0	533	1	FYN_MOUSE	P96888 mus musculus	Walch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,		
21	27	100.0	533	1	FYN_HUMAN	P06241 homo sapien	RASKO D., Buckles E.L., Liu S.-R., Boutin A., Hackett J., Stroud D.,		
22	27	100.0	536	1	FYN_XENIA	P13406 xenopus lae	Mayhew G.F., Rose D.J., Boutin A., Hackett J., Stroud D.,		
23	27	100.0	536	1	FYN_XTRE	P27446 xiphophorus	Mobley H.L.T., Donnenberg M.S., Blattner F.R.,		
24	27	100.0	609	1	GLMS_BUCBP	P59492 glucoamyl	"extensive mosaic structure revealed by the complete genome sequence of uropathogenic escherichia coli."		
25	27	100.0	617	1	DBP1_YEAST	P47849 saccharomyce	Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).		
26	27	100.0	678	1	UL06_HSV2H	P89429 herpes simp	[3]		
27	27	100.0	808	1	FTFB_DROME	P05192 drosophila	SEQUENCE FROM N. A.		
28	27	100.0	858	1	KCB1_RABBIT	Q9mz1 oryctolagus	SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;		
29	27	100.0	892	1	IFP2_YERKE	Q92bc2 yersinia pe	RX		
30	27	100.0	1536	1	Y984_THEME	Q0x079 thermotoga	MEDLINE=21156231; PubMed=11258796;		
31	24	88.9	44	1	RJ34_NEILSA	Q9jrl1 neisseria m	RA		
32	24	88.9	44	1	RJ34_RALSO	Q8j339 ralstonia s	RA		
33	24	88.9	44	1	Y4H_RULISN	P55686 rizobium s	RA		
ALIGNMENTS									
34	24	88.9	145	1	YPI2_AGRUT	YH10_NEIGO	RESULT 1		
35	24	88.9	170	1	YF64_METJA	NEF_TW2RO	ID		
36	24	88.9	233	1	YCBG_BACSU	MCRZ_METTA	AC		
37	24	88.9	250	1	YH10_NEIGO	062002 human immun	P3323;		
38	24	88.9	256	1	YH10_NEIGO	062002 human immun	01-FEB-1995 (Rel. 31, Last sequence update)		
39	24	88.9	266	1	YH10_NEIGO	062002 human immun	01-FEB-1995 (Rel. 31, Last sequence update)		
40	24	88.9	294	1	DAPA_AGRUT	09ug13 aerobacteri	DT		
41	24	88.9	299	1	YC68_SULRO	097400 sulfolobus	DE		
42	24	88.9	334	1	FEPD_ECOLI	P23876 escherichia	GN		
43	24	88.9	351	1	PSBD_PORPU	P51357 porphyra pu	OS		
44	24	88.9	362	1	AROB_BACUL	P3102 bacillus su	OS		
45	24	88.9	420	1	HC2C_MEGCR	P81732 megathura c	OS		

RT *Complete genome sequence of enterohemorrhagic Escherichia coli
RN O157:H7 and genomic comparison with a laboratory strain K-12.";
RT RL J. Bacteriol. 171:7135-7151(1997).
RP SEQUENCE FROM N.A.; STRAIN=301 / Serotype 2a;
RC SPECIES=S. flexneri;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin J., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng Z., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT *Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
through comparison with genomes of *Escherichia coli* K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC :-! SIMILARITY: BELONGS TO THE UP0131 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC
CC DR HAMAP; MF_00028; ; 1.
DR InterPro; IPR001047; Ribosomal_S8E.
DR Pfam; PF01201; Ribosomal_S8E; 1.
DR PRODOM; PD00568; Ribosomal_S8E; 1.
DR TIGRFAMS; TIGR03307; S8E; 1.
DR PROSITE; PS01193; RIBOSOMAL_S8E; 1.
DR Ribosomal protein; Complete proteome.
DR
DR EMBL; AE000807; AAB84713.1; -
DR PIR; D69125; D59125.
DR
DR EMBL; U14003; AAC7179.1; -
DR Pfam; PF0364; UPF0131; 1.
DR EMBL; AE01534; AANM5683.1; -
DR PIR; H6115; H6119.
DR PIR; H91278; H91278.
DR PIR; S56448; S56448.
DR Ecocfene; EG12516; ytfP.
DR InterPro; IPR005347; UPF0131.
DR PIR; H91278; H91278.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 113 AA; 12866 MW; A20C0PC94607CR8 CRC64;
Query Match 100.0%; Score 27; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RTRGG 5
Db 70 RTRGG 74
RESULT 2
RS8E_METTH ID RS8E_METTH STANDARD; PRT; 127 AA.
ID RS8E_METTH STANDARD; PRT; 127 AA.
AC 026309; DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 30S ribosomal protein S8E.
DE rpsB OR MJ0673.
GN Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcoidaceae; Methanocaldococcaceae.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=9633799; PubMed=8688057;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage R.A., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock G.K., Merrick J.M., Gocayne J.D.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuminaga J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hama M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
RT *jannaschii*.";
RT Science 273:1058-1073(1996).
RT
CC :-! SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC DR EMBL; U67514; AABBB667.1; -
DR PIR; A64304; A64304.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=9803514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Haang L., Keagle P., Lunn W., Pothier B., Qin D.,
RA Spadaccia R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwanji N., Caruso A., Bush D., Safer H., Patwell D., Prabakar S.,
RA McDougal S., Shimer G., Goyal A., Petrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nocella J., Reeve J.N.,
OC Metiobacteriaceae; Methanobacteriales;
OC NCBI_TaxID=187420;
RN

RP SEQUENCE FROM N.A. RX MEDLINE-91108372; PubMed-2273382; RA Vincent J.R.; Ueng P.P.; Lister R.M.; Larkins B.A.; "Nucleotide sequences of coat protein genes for three isolates of barley yellow dwarf virus and their relationships to other Luteovirus coat protein sequences"; J. Gen. Virol. 71:2791-2799(1990). [2] RP SEQUENCE FROM N.A. RX MEDLINE-92166764; PubMed-1538199; RA Ueng P.P.; Vincent J.R.; Kawata E.E.; Lei C.H.; Lister R.M.; RT "Nucleotide sequence analysis of the genomes of the MAV-PS1 and P-PAV isolates of barley yellow dwarf virus." RL J. Gen. Virol. 73:487-492(1992). CC -1- MISCELLANEOUS: THE N-TERMINAL REGION LIKE THOSE OF MANY PLANT VIRUS CAPSID PROTEINS IS HIGHLY BASIC. IT HAS BEEN SUGGESTED THAT THESE REGIONS MAY BE INVOLVED IN PROTEIN-RNA INTERACTION. -1- SIMILARITY: BELONGS TO THE LUTEOVIRUSES COAT PROTEIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: X117260; CAA35162.1; -. DR D11028; BAA01781.1; -. DR InterPro: IPR001517; Luteo_coat. DR pfam: PF00894; Luteo_coat; 1. DR PRINTS: PRO0915; LUTEOGICOMT. DR PRODOM: PD001068; Luteo_coat; 1. DR Coat_protein.

KW Coat protein.

SEQUENCE 199 AA; 21846 MW; 9005167499BC7E8E CRC64; Query Match 100.0%; Score 27; DB 1; Length 199; Best Local Similarity 100.0%; Pred. No. 35; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTRGG 5 Db 44 RTRGG 48

RESULT 6

CONT_BYDVM ID CONT_BYDVM STANDARD; PRT; 199 AA. AC P17966; "Rel. 16, Created" DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 01-NOV-1990 (Rel. 16, Last annotation update) DT 01-FEB-1994 (Rel. 23, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) AC P0574; P22801; "Rel. 09, Created" AC P0504636; PubMed-792509; RA Logue M.; Mollemans F.; Fiers W.; Contreras R.; RT "The two genes encoding yeast ribosomal protein s8 reside on different chromosomes, and are closely linked to the hsp70 stress protein genes SSA3 and SSA4.;" RT Yeast 10:1093-1100(1994). RL [2] RN SEQUENCE FROM N.A. RC STRAIN-S288C / AB972; RC Published-01169668; RA Dierrich F.S.; Mulligan J.T.; Hennessy K.M.; Yelton M.A.; Allen E.; RA Araujo R.; Aviles E.; Berno A.; Brennen T.; Carpenter J.; Chen E.; RA Cherry J.M.; Chung E.; Duncan M.; Guzman E.; Harrzeil G.; RA Hunnicke S.M.; Hyman R.W.; Kaysor A.; Komp C.; Lashkari D.; Lew H.; RA Lin D.; Mosedale D.; Nakabay K.; Namath K.; Norgren R.; Oefner P.; RA Oh C.; Petel F.X.; Roberts D.; Sehl P.; Schramm S.; Shogren T.; RA Smith V.; Taylor P.; Wei Y.; Boitstein D.; Davis R.W.; RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.;" RL Nature 387:78-81(1997). RN [3] RN SEQUENCE OF 69-199 FROM N.A. RC STRAIN-D510; RC MEDLINE-9105412; PubMed-2121731; RA Boorstein W.R.; Craig E.A.; RT "Structure and regulation of the SSA4 HSP70 gene of Saccharomyces cerevisiae;" RL J. Biol. Chem. 265:18912-18921(1990). RN [4] RN SEQUENCE OF 1-50. RA Okuda E.; Higao K.-I.; Itoh T.; RT "Yeast ribosomal proteins. VII. Isolation of two proteins and sequence characterization of twenty-four proteins from cytoplasmic RT ribosomes;" RL Mol. Gen. Genet. 195:544-546(1994). CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR S8 IN YEAST.

CC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: X53174; CAA3715.1; -. DR InterPro: IPR001517; Luteo_coat. DR Pfam: PF00894; Luteo_coat; 1. DR PR00915; LUTEOGICOMT. DR PRODOM: PD001068; Luteo_coat; 1. DR Coat_protein.

SEQUENCE 199 AA; 21846 MW; 9005167499BC7E8E CRC64; Query Match 100.0%; Score 27; DB 1; Length 199; Best Local Similarity 100.0%; Pred. No. 35; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RTRGG 5 Db 44 RTRGG 48

RESULT 7

RS8_YEAST ID RS8_YEAST STANDARD; PRT; 199 AA. AC P0574; P22801; "Rel. 09, Created" AC P0504636; PubMed-792509; RA Logue M.; Mollemans F.; Fiers W.; Contreras R.; RT "The two genes encoding yeast ribosomal protein s8 reside on different chromosomes, and are closely linked to the hsp70 stress protein genes SSA3 and SSA4.;" RT Yeast 10:1093-1100(1994). RL [2] RN SEQUENCE FROM N.A. RC STRAIN-S288C / AB972; RC Published-01169668; RA Dierrich F.S.; Mulligan J.T.; Hennessy K.M.; Yelton M.A.; Allen E.; RA Araujo R.; Aviles E.; Berno A.; Brennen T.; Carpenter J.; Chen E.; RA Cherry J.M.; Chung E.; Duncan M.; Guzman E.; Harrzeil G.; RA Hunnicke S.M.; Hyman R.W.; Kaysor A.; Komp C.; Lashkari D.; Lew H.; RA Lin D.; Mosedale D.; Nakabay K.; Namath K.; Norgren R.; Oefner P.; RA Oh C.; Petel F.X.; Roberts D.; Sehl P.; Schramm S.; Shogren T.; RA Smith V.; Taylor P.; Wei Y.; Boitstein D.; Davis R.W.; RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.;" RL Nature 387:78-81(1997). RN [3] RN SEQUENCE OF 69-199 FROM N.A. RC STRAIN-D510; RC MEDLINE-9105412; PubMed-2121731; RA Boorstein W.R.; Craig E.A.; RT "Structure and regulation of the SSA4 HSP70 gene of Saccharomyces cerevisiae;" RL J. Biol. Chem. 265:18912-18921(1990). RN [4] RN SEQUENCE OF 1-50. RA Okuda E.; Higao K.-I.; Itoh T.; RT "Yeast ribosomal proteins. VII. Isolation of two proteins and sequence characterization of twenty-four proteins from cytoplasmic RT ribosomes;" RL Mol. Gen. Genet. 195:544-546(1994). CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR S8 IN YEAST.

CC !- SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

DR EMBL: Z26879; CAA81525.1; -

DR EMBL: Z15833; CA8893.1; -

DR EMBL: U08839; AAB664657.1; -

DR EMBL: J05637; AAB663573.1; -

DR PIR: S45591; S45591.

DR SGD: S00016; R888A.

DR SGD: S0000904; R888B.

DR InterPro: IPR001047; Ribosomal_S8E.

DR Pfam: PF01201; Ribosomal_S8E; 1.

DR ProDom: PD005658; Ribosomal_S8E; 1.

DR TIGRFAMS: TIGR00307; S8E; 1.

DR PROSITE: PS01193; RIBOSOMAL_S8E; 1.

KW Ribosomal protein; Multigene family.

FT INIT_MER 0

FT CONFLICT 48 48 MW R -> K (IN REF. 4).

Qy SEQUENCE 199 AA: 22358 MW; DA9D3B0BAAE99B57 CRC64;

Qy 1 RTRGG 5

Db 46 RTRGG 50

RESULT 8

ID RS8_CAEEL STANDARD: PRT: 208 AA.

AC P48156; 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 40S ribosomal protein S8.

GN RPS-8 OR F42C5.8

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Plectoderaiae; Caenorhabditida;

OC NCBII_TaxID=2239; [1]

RN SEQUENCE FROM N.A.

RC STRAIN_Bristol N2;

RA Du Z.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

!- SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration -

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL: AF227516; AAK00652.1; ALT_INIT.

DR Genew; INSC:1553; SPRY4.

DR Pfam; PF05210; Sprotyt; 1.

KW Developmental protein; Membrane; Alternative splicing.

FT DOMAIN 97 107 POLY-SER.

FT CYS-RICH.

FT VARSPLIC 159 283 SVSSSSSTS -> CSATCLPAA (in Isoform C).

FT 97 106 /FT1d=VSP_005219.

FT VARSPLIC 107 299 Missing (in Isoform C).

FT /FT1d=VSP_005220.

Qy SEQUENCE 299 AA: 32541 MW; 105F6FBEB987B6C3 CRC64;

Qy 1 RTRGG 5

Db 66 RTRGG 70

SQ SEQUENCE 208 AA: 23750 MW; E1C38C2D21BB6275 CRC64;

Qy 1 RTRGG 5

Db 47 RTRGG 51

RESULT 9

ID SPY4_HUMAN STANDARD: PRT: 299 AA.

AC Q9C004; Q9C003; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sprouty homolog 4 (SPRY4).

GN SPRY4.

OS Homo sapiens (Human).

RA Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

RA von dem Borne A.E.C., Pannekoek H., de Vries C.J.M.;

RT Identification of a novel human Sprouty homolog. *

RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

CC [1] FUNCTION: MAY FUNCTION AS AN ANTAGONIST OF FIBROBLAST GROWTH FACTOR (FGF) PATHWAYS AND MAY NEGATIVELY MODULATE RESPIRATORY TISSUE-UNMILICR arter.

CC ORGANogenesis (BY SIMILARITY).

CC -I- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms*2;

CC Name*2;

CC Isoform-Q9C004-1; Sequence-Displayed;

CC Name*2;

CC Isoform-Q9C004-2; Sequence=vSP_006319, VSP_006320;

CC NOTE--No experimental confirmation available;

CC -I- DOMAIN: THE CYS-RICH DOMAIN IS RESPONSIBLE FOR THE LOCALIZATION OF THE PROTEIN TO THE MEMBRANE RIBOSOME.

CC -I- SIMILARITY: BELONGS TO THE SPROUTY FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration -

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL: AF227517; AAK00653.1; -

DR Genew; INSC:1553; SPRY4.

DR Pfam; PF05210; Sprotyt; 1.

KW Developmental protein; Membrane; Alternative splicing.

FT DOMAIN 159 283 CYS-RICH.

FT VARSPLIC 97 106 SVSSSSSTS -> CSATCLPAA (in Isoform C).

FT /FT1d=VSP_005219.

FT VARSPLIC 107 299 Missing (in Isoform C).

FT /FT1d=VSP_005220.

Qy SEQUENCE 299 AA: 32541 MW; 105F6FBEB987B6C3 CRC64;

Qy 1 RTRGG 5

Db 66 RTRGG 70

RESULT 10		RN
ID Y942_SULSO	STANDARD:	PRT: 310 AA.
097H1;		
DT 28-FEB-2003 (Rel. 41, Created)		
DT 28-FEB-2003 (Rel. 41, Last sequence update)		
DT 28-FEB-2003 (Rel. 41, Last annotation update)		
DE HYPOTHETICAL TRANSCRIPTIONAL REGULATORY PROTEIN SS00942.		
GN SS00942.		
OS <i>Sulfolobus solfataricus</i> .		
OC Archaea: Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;		
OC Sulfolobus.		
OX NCBI_TAXID=2287;		
RR [1]		
RP SEQUENCE FROM N_A.		
RC STRAIN=ATCC 35092 / DSM 1617 / P2;		
RA MEDLINE=21322965; PubMed=11481431;		
RA She C., Singh R.K., Confalonieri P., Zivanovic Y., Allard G.,		
RA Awazey M.J., Chan-Weiner C.C.Y., Clausen I.G., Curtis B.A.,		
RA De Mors A., Krause G., Fletcher C., Gordon P.M.K.,		
RA Heilmann de Jong I., Jeffries C.J., Medina N., Peng X.,		
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,		
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,		
RA Garrett R.A., Regan M.A., Sensen C.W., Van der Oost J.,		
RT *The complete genome of the crenarchaeon <i>Sulfolobus solfataricus</i> P2.;		
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).		
CC -1- SIMILARITY: BELONGS TO THE PSX(XRE) FAMILY OF TRANSCRIPTIONAL		
CC REGULATORS. ARCHAEAL 1 SUBFAMILY.		
CC -----		
CC This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC the European Bioinformatics Institute. There are no restrictions on its		
CC use by non-profit institutions as long as its content is in no way		
CC modified and this statement is not removed. Usage by and for commercial		
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC -----		
CC DR EMBL: AY013584; AAC42537.1; -.		
CC DR EMBL: AL603642; CAG48596.1; -.		
CC DR PIR: B95866; D95866.		
CC DR Interpro: IPR000847; HTH_LysR.		
CC DR Interpro: IPR005119; LysR_Subst.		
CC DR Pfam: PF00126; HTH_1; 1.		
CC DR Pfam: PF03466; LysR_substrate; 1.		
CC DR PROSITE: PS00044; HTH_LysR_FAMILY; 1.		
CC DR Transcription regulation; Activator; DNA-binding; Plasmid;		
CC DR Complete proteome.		
CC FT DNA_BIND 21 40 H-T-H MOTIF (POTENTIAL).		
CC SQ SEQUENCE 310 AA; 35385 MW; F8DD43C3C069DA39 CRC64;		
CC -----		
CC Query Match 100.0%; Score 27; DB 1; Length 310;		
CC Best Local Similarity 100.0%; Pred. No. 53;		
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CC -----		
CC RESULT 11		
CC CBR1_RHIME STANDARD: PRT: 313 AA.		
CC P58332; Q9EXV3; [1]		
CC DT 28-FEB-2003 (Rel. 41, Created)		
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR OR RBB0196 OR SWR20203.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>).		
CC Plasmid pSymB (megaplasmid 2).		
CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;		
CC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 11		
CC CBR1_RHIME STANDARD: PRT: 313 AA.		
CC P58332; Q9EXV3; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		
CC OS <i>Rhizobium meliloti</i> (<i>Sinorhizobium meliloti</i>); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.		
CC NCBI_TAXID=382;		
CC -----		
CC RESULT 12		
CC CBR2_RHIME STANDARD: PRT: 313 AA.		
CC P56885; [1]		
CC DT 30-MAY-2000 (Rel. 39, Created)		
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)		
CC DE RUBISCO OPERON TRANSCRIPTIONAL REGULATOR.		
CC CBBR.		

CC RBGULATORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR InterPro; IPRO000594; Thif_F_domain.

CC DR Pfam; PF00556; ldh; 1.

CC DR Pfam; PF02866; ldh_C; 1.

CC DR PRINTS; PR00056; LIDHDIGNEASE.

CC DR PROSIE; PS00054; L_LDH; FALSE_NEG.

CC KW Oxidoreductase; NAL; Glycolysis.

CC FT ACT_STNE 172 172 [ACCEPTS A PROTON DURING CATALYSIS (BY SIMILARITY)].

CC FT FT 436AC40F87A07A19 CRC64;

CC DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

CC DR InterPro; IPRO00847; HTH_LYSR.

CC DR Pfam; PF00125; HTH_1; 1.

CC DR Pfam; PF03466; LYSR_substrate; 1.

CC DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

CC DR InterPro; IPRO05119; LYSR_subst.

CC DR DNA_BIND 21 40 H-T-H MOTIF (POTENTIAL).

CC DR SEQUENCE 313 AA; 34192 MW; 818C5F5FC0FCED24 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 313; Best Local Similarity 100.0%; Pred. No. 54; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 53 RTRGG 57

RESULT 13

ID LDH_BOTBR STANDARD; PRT; 316 AA.

ID P93052; 316 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 15-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH).

OS Botryococcus braunii (Green alga)

OC Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Chlorococcales; Botryococaceae; Botryococcus.

OX NCBI_TAXID=8881;

RN [1]

RP SEQUENCE FROM N_A.

RC STRAIN=Race A;

RA Vioque J., Strakova T., Kolattukudy P.E.;

RT "Malate dehydrogenase gene from *Botryococcus braunii*." Submitted (DPC-1996) to the EMBL/GenBank/DBJ databases. [2]

RN PROBABLE FUNCTION.

RA Louis A., Ollivier E., Aude J.-C., Risler J.-L.;

RT "Massive sequence comparisons as a help in annotating genomic sequences." Submitted (MAR-2001) to the SWISS-PROT data bank.

RL DR

CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = Pyruvate + NADH.

CC -!- PATHWAY: Aerobic glycolysis; final step.

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.

CC -!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A MALATE DEHYDROGENASE.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR InterPro; IPRO01238; AACC40997_1.

CC DR HSSP; P36325; LASH.

CC DR InterPro; IPRO01803; Orbi_VP7_capsid.

CC DR Pfam; PF00897; Orbi_VP7; 1.

CC DR PRINTS; PR00053; VP7CAPSID.

CC DR ProDom; PD005062; Orbi_VP7_capsid; 1.

CC KW Core protein; Glycoprotein.

CC FT CARBOHYD 45 N-LINKED (GLCNAC) (POTENTIAL).

CC FT SEQUENCE 349 AA; 37828 MW; 7FE1731D1152E2C CRC64;

Query Match 100.0%; Score 27; DB 1; Length 349; Best Local Similarity 100.0%; Pred. No. 60; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 147 RTRGG 151

RESULT 14

ID VP7_AHSV6 STANDARD; PRT; 349 AA.

ID VP7_AHSV6 349 AA.

DT 071027; 349 AA.

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE VP7 core protein (VP7 antigen) (Capsid protein VP7).

GN S7

OS African horse sickness virus 6 (AHSV-6) (African horse sickness virus (serotype 6)).

OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.

OX NCBI_TAXID=86060;

RN [1]

RP SEQUENCE FROM N_A.

RX MEDLINE-9827831; Published-9611769;

RA Williams C.F., Inoue T., Lucas A.M., Zanotto P., Roy P.;

RT "The complete sequence of four major structural proteins of African horse sickness virus serotype 6: evolutionary relationships within and between the orbiviruses."

RT Virus Res. 53:53-73 (1998).

CC -!- FUNCTION: MAJOR STRUCTURAL CORE PROTEIN; BINDS TO STRUCTURAL PROTEIN VP3; CONSTITUTES THE SURFACE OF THE AHSV CORE.

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SIMILARITY: BELONGS TO THE REOVIRUSES VP7 FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR InterPro; IPRO01238; AACC40997_1.

CC DR HSSP; P36325; LASH.

CC DR InterPro; IPRO01803; Orbi_VP7_capsid.

CC DR Pfam; PF00897; Orbi_VP7; 1.

CC DR PRINTS; PR00053; VP7CAPSID.

CC DR ProDom; PD005062; Orbi_VP7_capsid; 1.

CC KW Core protein; Glycoprotein.

CC FT CARBOHYD 45 N-LINKED (GLCNAC) (POTENTIAL).

CC FT SEQUENCE 349 AA; 37828 MW; 7FE1731D1152E2C CRC64;

Query Match 100.0%; Score 27; DB 1; Length 349; Best Local Similarity 100.0%; Pred. No. 60; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTRGG 5

Db 147 RTRGG 151

RESULT 15

VP7_AHSV9
 ID VP7_AHSV9 STANDARD: PRT; 349 AA.
 AC 086729; 011856;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VP7 core protein (VP7 antigen) (Capsid Protein VP7).
 GN S7.
 OS African horse sickness virus 9 (AHSV-9) (African horse sickness virus
 OS (serotype 9)).
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID:10897;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE="4157018; PubMed=8113344;
 RA Wade-Evans A.M.; Woolhouse T.; O'Hara R.; Hamblin C.;
 RT "The use of African horse sickness virus VP7 antigen, synthesised in
 bacteria, and anti-VP7 monoclonal antibodies in a competitive
 RT ELISA.";
 RL J. Virol. Methods 45:179-188(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE="8131959; PubMed=9472617;
 RA Maree S.; Durbach S.; Huismans H.;
 RT "Intracellular production of African horse sickness virus core-like
 RT particles by expression of the two major core proteins, VP3 and VP7,
 in insect cells.";
 RL J. Gen. Virol. 79:333-337(1998).
 CC FUNCTION: MAJOR STRUCTURAL CORE PROTEIN; BINDS TO STRUCTURAL
 CC PROTEIN VP3; CONSTITUTES THE SURFACE OF THE AHSV CORE.
 CC -I- SUBUNIT: Homotimer (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE REOVIRUSES VP7 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to licensee@isb-sib.ch).
 CC
 DR EMBL; S69829; AAB29954; 1; -;
 DR EMBL; U90337; AAC04609; 1; -;
 DR HSSP; P36325; IAHB.
 DR InterPro; IPR001803; Orbi_VP7_capsid.
 DR Pfam; PF00897; Orbi_VP7; 1.
 DR PRINS; PR00903; VP7CAPSID.
 DR Prodrom; PR005062; Orbi_VP7_capsid; 1.
 KW Core protein; Glycoprotein.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC,) (POTENTIAL).
 FT CONFLICT 5 5 A -> R (IN REF. 2).
 FT 80 80 V -> I (IN REF. 2).
 SQ SEQUENCE 349 AA.: 37814 MW: 7E99EE9DD1137CC3 CRC64:
 Query Match 100.0%; Score 27; DB 1; Length 349;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 DB 147 RTRGG 151

Search completed: September 9, 2003, 23:32:17
 Job time : 19.5 secs

Gencore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2003, 23:28:08 ; Search time 75 Seconds
(with alignments) updates/sec

Title: US-09-967-003-3

Perfect score: 27

Sequence: 1 RTGG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBBL23

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriop:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	27	100.0	19	6 Q9SGH0
2	27	100.0	51	16 Q8DCV4
3	27	100.0	61	16 Q8DCV5
4	27	100.0	64	3 Q04333
5	27	100.0	85	11 Q8R245
6	27	100.0	111	12 Q81TG7
7	27	100.0	114	16 Q8XGN0
8	27	100.0	121	4 Q9HR05
9	27	100.0	121	10 Q8LTM4
10	27	100.0	125	5 Q8SW51
11	27	100.0	125	10 Q8RYW2
12	27	100.0	127	13 Q90W6B
13	27	100.0	141	17 Q8TYG7
14	27	100.0	143	16 Q8PDC2
15	27	100.0	145	16 Q9Kb7
16	100.0	145	16 Q9JX84	neisseria m

RESULT 1	SEQUENCE FROM N.A.	PRELIMINARY:	PRT:	19 AA.
Q9BGH0	Larkin D., Kuznetsov S., Zhdanova N. ; "Mapping of porcine HLR1 gene."			
ID Q9BGH0;	Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.			
AC Q9BGH0;				
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE RNA helicase 1 (Fragment).				
GN HLR1.				
OS Sus scrofa (Pig).				
OC BakaYota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX [1]				
RN				
RP				
RA				
RT				
RL				
DR EMBL; AR314825; AAC01168.1; -				
KW Helicase.				
FT NON_TER	1	1		
FT	19	19		
SQ SEQUENCE	19 AA:	2224 MW:	AE2928DC68DD0F66D CRC64:	
Query Match	100.0%	Score 27:	DB 6;	Length 19;
Best Local Similarity	100.0%	Score 27:	DB 6;	Length 19;
Matches	5	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	
Db	5	RTGG 9.		

RESULT 2	PRELIMINARY:	PRT:	51 AA.
Q8DCV4			
ID Q8DCV4			
AC Q8DCV4;			
DT 01-MAR-2003 (TREMBLrel. 23, Created)			
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)			

DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	RP	SEQUENCE FROM N.A.
OC	Conserved hypothetical protein.	RC	STRAIN=D11;
OS	Vibrio vulnificus.	RA	Kutulina A.I., Seregina S.A., Tikhomirova L.P., Kryukov V.M.;
OC	Bacterium; Proteobacteria; Gammaproteobacteria; Vibrionales;	RA	WV11889.
OC	vibroniae; Vibrio.	RT	"Nucleotide sequence of <i>Haemulon polymorpha</i> DNA region complementing
NCBI_TAXID=672;	[1]	RT	DNA";
RN	SEQUENCE FROM N.A.	RL	"Nucleic Acids Res. 0:0-0(0);
RC	STRAIN=CMP6;	DR	EMBL: X58862; CAA41667.1; -;
RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	SQ	SEQUENCE 64 AA; 7488 MW; 23D2D20586F48C54 CRC64;
RC	Choy H.E.;	Query Match	100.0%; Score 27; DB 3; Length 64;
RT	*Complete genome sequence of <i>Vibrio vulnificus</i> CMP6.*;	Best Local Similarity	100.0%; Pred. No. 75;
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.	Matches	Mismatches 0; Indels 0; Gaps 0;
KW	Hypothetical protein; Complete proteome.	QY	1 RTRGG 5
SQ	SEQUENCE 51 AA; 5429 MW; O168RAD224CB3E5 CRC64;	Db	12 RTRGG 16
RESULT 3		RESULT 5	
QDCCV5	PRELIMINARY;	QDCCV5	PRELIMINARY;
ID	PRT; 61 AA.	ID	PRT; 86 AA.
AC	08DCV5;	AC	08R245
DT	01-MAR-2003 (TREMBLrel. 23, Created)	DT	01-JUN-2002 (TREMBLrel. 21, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Conserved hypothetical protein.	DE	Hypothetical 9.2 kDa protein.
GN	WIL287.	OS	Mus musculus (Mouse).
OS	Vibrio vulnificus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	Vibrionaceae; Vibrio.	OX	NCBI_TAXID=10950;
OC	NCBI_TAXID=672;	RN	[1]
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=CMP6;	RA	Strausberg R.;
RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RT	*Complete genome sequence of <i>Vibrio vulnificus</i> CMP6.*;	DR	EMBL: BC022589; AAC022599.1; -;
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.	KW	Hypothetical protein.
DR	EMBL: AE016801; AA009742.1; -;	SQ	SEQUENCE 86 AA; 9225 MW; ACD6FEDAF9PB3F50 CRC64;
RN	SEQUENCE FROM N.A.	Query Match	100.0%; Score 27; DB 11; Length 86;
RC	Vibrio vulnificus.	Best Local Similarity	100.0%; Pred. No. 1e+02;
RA	Choy H.E.;	Matches	Mismatches 0; Indels 0; Gaps 0;
RT	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.	QY	1 RTRGG 5
RL	[1]	Db	55 RTRGG 59
DR	EMBL: AE016801; AA009742.1; -;	RESULT 6	
KW	Hypothetical protein; Complete proteome.	ID	091TG7
SQ	SEQUENCE 61 AA; 6523 MW; 8036B0BDB2B0A19 CRC64;	AC	091TG7;
Query Match	100.0%; Score 27; DB 16; Length 61;	DT	01-DEC-2001 (TREMBLrel. 19, Created)
Best Local Similarity	100.0%; Pred. No. 71;	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
QY	1 RTRGG 5	DE	T129.
Db	54 RTRGG 58	OS	Tupaia herpesvirus.
RESULT 4		OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
QDCC33	PRELIMINARY;	OC	Betaherpesvirinae.
ID	PRT; 64 AA.	OX	NCBI_TAXID=10397;
AC	004333;	RN	[1]
DT	01-NOV-1996 (TREMBLrel. 01, Created)	RP	SEQUENCE FROM N.A.
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	RC	STRAIN=2;
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	RA	MEDLINE:21211637; PubMed=11312357;
DE	dB DNA for region containing 9 open reading frames.	RT	"Analysis and Characterization of the complete Genome of <i>Tupaia</i> (Tree
OS	<i>Pichia</i> angusta (Reast) <i>Hansenula polymorpha</i> .	RT	Shrew) Herpesvirus";
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	RL	J. Virol. 75:4545-4870(2001).
OC	Saccharomycetidae; Saccharomycetaceae; <i>Pichia</i> .	RN	[2]
NCBI_TAXID=4905;	[1]	RP	SEQUENCE FROM N.A.
DR	Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.	RA	Daraí G.; Bahr U.;
DR	EMBL: AF281817; AAC57180.1; -;	RL	Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 [2] SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE=1575510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornilliat E., Melenier G., Thomarat F.,
 PRENSIER G., Barbe V., Peyrette J., Brottier P., Wincker P.,
 RA Delbac F., El Aloui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vives C.P.,
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi";
 RL Nature 414:450-453(2001).
 EMBL: AL19043; CAC26206.;
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR SMART: SM00359; Hox; 1.
 DR PROSITE: PS50071; HOMEOBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 SQ SEQUENCE 125 AA; 14342 MW; 6CCD4F8E8A61C1309 CRC64;
 Query Match 100.0%; Score 27; DB 5; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTRGG 5
 Db 94 RTRGG 98

RESULT 11
 Q8RYW2
 ID Q8RYW2
 PRELIMINARY; PRT; 125 AA.
 AC Q8RYW2;
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE OSJNBA0066C06_16 protein.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nippobare(Ga3) genomic DNA, chromosome 1, BAC
 clone:OSJNBA0066C06.;"
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AP003933; BAB80643.1; -.
 DR Gramene: Q8RYW2; -.
 SQ SEQUENCE 125 AA; 13346 MW; 3698106B2FCA76C CRC64;
 Query Match 100.0%; Score 27; DB 10; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Db 47 RTRGG 51

RESULT 12
 Q9W6B
 ID Q9W6B
 PRELIMINARY; PRT; 127 AA.
 AC Q9W6B;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

Query Match 100.0%; Score 27; DB 17; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Db 84 RTRGG 88

RESULT 13
 Q8YIG7
 ID Q8YIG7
 PRELIMINARY; PRT; 141 AA.
 AC Q8YIG7;
 DT 01-JUN-2002 (TREMBLrel. 21, created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Oncharchaeotal protein conserved in archaea.
 GN MK0332.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezhevaya K.V., Makrova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shatkova V.V., Belova G.I., Aravind L.,
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozhevnikov S.A.;
 RT "The complete genome of hyperthermophilic Methanopyrus kandleri AV19
 and monophyly of archaeal methanogens";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
 DR EMBL: AE010331; AAC01547.1; -.
 KW Complete proteome.
 SQ SEQUENCE 141 AA; 15678 MW; CEDC61208CD6GAFF CRC64;
 Query Match 100.0%; Score 27; DB 17; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTRGG 5
 Db 84 RTRGG 88

RESULT 14
 Q8PC2
 ID Q8PC2
 PRELIMINARY; PRT; 143 AA.
 AC Q8PC2;

DT	01-OCT-2002 (TREMBrel. 22, Created)	DR	TIGR: NMB0247;
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)	KW	Hypothetical protein; Complete proteome.
DE	VIRK protein.	SQ	SBQUENCE 145 AA; 16606 MW; 105PEFR8581CD138 CRC64;
GN	VIRK OR XCC0418.	Query Match	100.0%; Score 27; DB 16; Length 145;
OS	Xanthomonas campestris (pv. campestris)	Best Local	Similarity 100.0%; Pred. No. 1.7e+02;
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC	Xanthomonadaceae; Xanthomonas.		
OX	NCBI_TAXID_340;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC			
RX			
RA	STRAIN=NCC 33913 / NCPPB 520B;		
RX	MEDLINE=22022145; PubMed=12024217;		
RA	da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,		
RA	Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,		
RA	Alves L.M.C., do Amaral M.A., Bertolini M.C., Camargo L.E.A.,		
RA	Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,		
RA	Cicarelli R.M., Coutinho L.L., Cursino-Santos J.R., El-Borry H.,		
RA	Faría J.B., Ferreira A.J.S., Ferreira M.I.T.,		
RA	Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,		
RA	Katsuyama A.M., Kishii L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,		
RA	Locardi E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,		
RA	Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,		
RA	Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,		
RA	Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,		
RA	Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,		
RA	Trindade dos Santos D., Truffi D., Tsai S.M., White F.F.,		
RA	Setubal J.C., Kitajima J.P.;		
RT	*Comparison of the genomes of two <i>Xanthomonas</i> pathogens with differing		
RT	host specificities.		
RL	Nature 417:459-463(2002);		
DR	EMBL; AR012139; AA439736.1; -.		
KW	Complete proteome.		
SQ	SEQUENCE 143 AA; 15523 MW; 83E620974B31B9C7 CRC64;		
Query Match	100.0%; Score 27; DB 16; Length 143;		
Best Local	Similarity 100.0%; Pred. No. 1.7e+02;		
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 RTRGG 5		
Db	61 RTRGG 65		
RESULT	15		
09K1B7			
ID	09K1B7 PRELIMINARY; PRT; 145 AA.		
AC			
DT	01-OCT-2000 (TREMBrel. 15, Created)		
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)		
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)		
DE	Hypothetical protein NMB0247.		
GN	NMB0247.		
OS	<i>Neisseria meningitidis</i> (serogroup B).		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	<i>Neisseriaceae</i> ; <i>Neisseria</i> .		
OX	NMBI_TAXID=491;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MC58 / Serogroup B;		
RX	MEDLINE=20175755; PubMed=107110307;		
TEXT	Teitelbaum H., Saunders N.J., Heidelberg J.J., Jeffries A.C., Nelson K.E.,		
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,		
RA	Nelson W.C., Sutton M.L., DeBoy R.R., Peterson J.D., Hickey E.K.,		
RA	Hart D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,		
RA	Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,		
RA	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vaithyanathan J.,		
RA	Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,		
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,		
RT	'Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58.'		
RL	Science 287:1809-1815(2000);		
DR	EMBL; AE002381; AAB40701.1; -.		